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Minimum DB:
Maximum DB:
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Listing first 45 summaries
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Sequence:
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Gapop 10.0 , Gapext 0.5
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1401
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12.7
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US-09-738-626-3905

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                                                       US-10-007-267-11

US-09-815-242-4950

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US-09-767-041-22

US-09-815-242-5714

US-09-815-242-12474

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                                                 Sequence 36, Appl
Sequence 274, Appl
Sequence 12474, A
Sequence 29, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 305, Ap
Sequence 31, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 4950, Ap
Sequence 39, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 31, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 33, Appl
Sequence 34, Appl
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                                      Sequence 35, App
   Sequence
Appli
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92.5	92.5	94.5	96.5	100	100	102	105	107.5	107.5	108.5	108.5	123.5	128	128	129	131	132	134.5	141	144.5	144.5	145.5	146.5	149.5	150	
6.6	6.6	6.7	6.9	7.1	7.1	7.3	7.5	7.7	7.7	7.7	7.7	8.8	9.1	9.1	9.2	9.4	9.4	9.6	10.1	10.3	10.3	10.4	10.5	10.7	10.7	
269	256	398	395	317	317	440	313	272	272	303	270	418	337	337	389	243	210	674	303	297	281	345	301	972	187	
10	10	0	12	10	10	9	10	10	10	10	10	10	12	12	10	9	10	10	10	10	10	9	10	9	12	
US-09-767-041-41	US-09-925-301-883	US-09-741-669-430	US-10-042-523-4	US-09-934-868-38	US-09-934-899-18	US-09-902-525-46	US-09-900-038A-1	US-09-934-868-32	US-09-934-899-12	US-09-765-272-202	US-09-765-272-198	US-09-816-028A-33	US-10-007-267-12	US-10-007-267-5	US-09-816-028A-34	US-09-738-626-4733	US-09-767-041-47	US-09-765-272-200	US-09-816-028A-29	US-09-816-028A-31	US-09-765-272-196	US-09-738-626-3894	US-09-816-028A-27	US-09-879-959-10	US-10-074-527-4	
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; NAME/KEY: misc_feature
; OTHER INFORMATION: CPS1K
US-09-767-041-36
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US-09-767-041-36
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SEQ ID NO 36
LENGTH: 278
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PRIOR FILING DATE: 1999-0
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/767,041
CURRENT FILING DATE: 2001-01-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Streptococcus suis
    122 DRVDASGHFLTAEPLPTN----
                                  110 LGDHAASHLVYGDVVMRSTKSRHAGPFDLDRLLFETNLC------HQSI-----FYRR 156
                                                                        62 IRYFKKENGGLSDARNYGISRAKGDYLAFIDSDDFIHSEFIQRLHEAIERENALVAVAGY 121
                                                                                                               62 LVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLY------EPTTLAQVAAF 109
                                                                                                                                                     3 TISKISITVPIYNVEKYLSKCIDSIVNQTYKHIEILLVNDGSTDNSEEICLAYAKK-DSR 61
                                                                                                                                                                                            2 TAPVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSR 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn version 3.0
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23.6%; Pred. No. 3.6e-11;
rative 47; Mismatches 93;
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; NAME/KEY: misc_feature
; OTHER INFORMATION: CPS2K
US-09-767-041-22
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Best Local S
Matches 68
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SEQ ID NO 22
LENGTH: 332
TYPE: PRT
                              Sequence 5714, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION:
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 APPLICANT:
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PRIOR FILING DATE: 1998-07-22
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CURRENT FILING DATE: 2001-01-22
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                                                                                                                                                                                                                                                                                                                                                           124 SGHFLTAEPLPTN------QAVLSGRNVCKKLLEADGHRFVVAWNKLYKKELFD-
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mes 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                            64 KENGGLSDARNYGISRAKGDYLAFIDSDDFIHSEFIQRLHEAIERENALVAVAGYDRVDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 SIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLVVHS 66
                                                                                                                                                       KQLKQNKRLAL 294
                                                                                                                                                                                                                       HCLLEFQNERMDFYESRGDKELLLECYRSFLAFAVLFLGKYNHWLSKQQKKLQTLFRIVY 283
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Ohlsen, Kari L.
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21.9%;
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Pred. No. 5.9e-11;
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; ORGANISM: Staphylococcus aureus 
US-09-815-242-5714
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Best Local Similarity
Matches 51; Conserv
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SEQ ID NO 5714
                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12474, Application US/09815242
                                            CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
                                                                                     CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                       APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                         FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Haselbeck, Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GDVVMRSTKSRHAGPFDLDRLLFETNLCHQSIFY 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RLVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVY 120
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Zyskind, Judith W.
                                                                                                                                                                                                                                                   Carr, Grant
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Trawick, John D.
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Pred. No. 2.9e-10;
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PRIOR FILING DATE:

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US-09-815-242-12474
                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 150
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Best Local Similarity
                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MacBeth, Kyle
APPLICANT: MacBeth, Kyle
TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226, AND
TITLE OF INVENTION: 05764,
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE FAMILY MEMBERS AND USES THEREFOR
FILE REFERENCE: 38155-20034.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-0
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                                                                                                                                                                                                                                                                                                                                              FEATURE:
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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ORGANISM: Artificial Sequence
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124 VMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRELFD 160
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                                            60 LEENLGLAAARNAGLKHATGDYDYIAFLDADDEV--PDWLEKLLELLEKNGAD-IVIGRV 116
                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                     SIIIPTENAAVTLQACLGSIVGQ-TYREVEVVLVDGGSTDRTLDIANSFRPELGSRLVVH 65
                                                                                  SGPDDGPYDAMNRGVGVATG--EWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYGDV 123
                                                                                                                             SIIIPTYNEEKYLEECLESLLNQTTYENFEIIVVDDGSTDGTVEILEEYAKDPRIR-VIR 59
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5. US20020107376A1
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                                                                                                                                                                                                                 11.8%; Score 165.5; DB 10 ilarity 35.0%; Pred. No. 4.3e-10; Conservative 26; Mismatches 63;
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3ER: US 60/229,300
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Mismatches
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SEQ ID NO 4202
LENGTH: 251
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                                                                              213 ALMGVRQSFIRLVRGFYTIK--IAWKREPVHQRLESR 247
                                                                                                                                                                                                                                                  111 ETPGRTIVALTGT---GSFDIPGRMGEWLALCYLGA-YRWSTKQALGHYPI------
                                                                                                                                                                                                                                                                                           118 LYYGDYVMRSTKSRHAGPFDLDRLLFE-TNLCHQSIFYRRELFDGIGPYNLRYRVWADWD 176
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                                                                                                                                                                                                                                                                                                                                  57 MGAR-VVHE-PLQGITWASAAGYNSARGDLIVRFDA-DCVIPPDHLSQVNAIWN---RTE 110
                                                                                                                                                                                                                                                                                                                                                                       58 LGSRLYVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASH 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
mes 76; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MTAPV---FSIIIPTENAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPE 57
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                                                                                                                                                                                                      FNIRCESNPALITRYM-----DVVISE---YNDM-TGESMRQGTDKEERKRLPMYE---
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TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
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                                                                                                                                                                 -FGSNSVISRQWWEDVKDQITLSETFVHEDMYFSFFVRPHETVWFEKNLKLIMHPR 212
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OCHIAI, KEIKO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                          -WVAGWETCRRMLAFLKDKENRRLALR 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.8%; Score 165; DB 9; Length 251; 27.4%; Pred. No. 1e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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15;

Sequence 21, Application US/09767041 Patent No. US20020055168A1

GENERAL INFORMATION:

TITLE OF INVENTION:

Smith, Hilda

FILE REFERENCE: APPLICANT:

CURRENT APPLICATION NUMBER: US/09/767,041
CURRENT FILING DATE: 2001-01-22

2183-4726

STREPTOCOCCUS SUIS VACCINES AND DIAGNOSTIC TESTS

PRIOR APPLICATION NUMBER:

PCT/NL99/00460

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                                                                                                                                    US-09-738-626-3905
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; OTHER INFORMATION: CPS2J
US-09-767-041-21
                                                                                                                                                                               SOFTWARE: PatentIn ver.
SEQ ID NO 3905
LENGTH: 274
                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
SEQ ID NO 21
                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: UD/07/10, CURRENT FILING DATE: 2000-12-18 PRIOR APPLICATION NUMBER: UP 99/377484 PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: JP 00/280988 PRIOR FILING DATE: 2000-08-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 332
TYPE: PRT
                                                                                                                                                ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Streptococcus suis
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.ication No. US20020197605A1
;RAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 GPDDGPYDAMNRGVGVATGEWVLFLGADD-----TLYEPTTLAQ------VAAF 109
                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 LPNGGVSNARNYGIKNSTANYIMFVDSDDIVDGNIVESLY--TCLKENDSDLSGGLLATF 121
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                               2 TAPVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: EP9
FILING DATE: 1998-07-22
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: JP 00/159162 FILING DATE: 2000-04-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGNYQESEL 130
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SAPLISVVIPTIAYDEYCSQSIKSVCEQNYENWQIVLVLDGAPIK--DVPQWVKEH--ER 59
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/738,626
                                                                                                                                                                                                                                                                                                                                                                                                                                                  YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAKAGAWA, SATOSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                   OZAKI, AKIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                      IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIZOGUCHI,
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                                                                                 11.6%;
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Pred. No. 2.4e-09;
                                                                 Pred. No. 2.1e-09;
2; Mismatches 108
                                                                                                Score 162.5;
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                                                                                                DB 9;
                                                                   108;
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                                                               Gaps
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Query Match
Best Local Similarity
Watches 32; Conserve
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; OTHER INFORMATION: N-terminal part of CPS2J
US-09-767-041-51
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US-09-767-041-51
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                                                                                                                                                                                                                                                      RESULT 10
                                                                                                                                                         Sequence 3, Application US/10007267
Patent No. US/20020127/682A1
GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 51, Application US/09767041
Patent No. US20020055168A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/767,041
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: PCT/NL99/0046
PRIOR FILING DATE: 1999-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
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PRIOR APPLICATION NUMBER: EPYPRIOR APPLICATION NUMBER: 1998-07-2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Streptococcus suis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 I---LKRRMELASFLKRSPVRQIFL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 NLRYRVWADWDFNIRCFSNPALITRYMDVVISEYNDMTGFSMRQGTDKEFRKRLPMYFWV 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 --IICVATKTKHINEHGKIFGQSADLPTSQDIRQILLVKNPIIHSSVMYRKQVVEQIGGY 171
                                                                                                                                                                                                                                                                                                               64 LPNGGVSNARNYGIKNSTANYIMFVDSDD 92
                                                                                                                                                                                                                                                                                                                                               67 GPDDGPYDAMNRGVGVATGEWVLFLGADD 95
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                                                                                                                                                                                                                                                                                                                                                                                                                              7 SIIIPTENAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLVVHS 66
                                                                                                                                                                                                                                                                                                                                                                                            5 SIIVPIFNTEKYLRECLDSIISQSYTNLEILLIDDGSSDSSTDICLEYAEQDG~RIKLFR 63
                                                                            NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS:
                                                                                                                                     APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGWETCRRM--LAFLKDKENRRLAL 248
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                                        STREET:
                                                          ADDRESSEE: Klauber & Jackson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith, Hilda
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New Jersey
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                                    411 Hackensack Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.48;
36.08;
                                                                                                                   OLIGOSACCHARIDES,
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Pred. No. 1.
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COUNTRY: USA

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RESULT 11
US-10-007-267-11
                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/10007267
Patent No. US20020127682A1
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 MGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAF----FPFGNPIHNNTMIMRRS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 VIDG----GLRYDTERDW 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 LFDGIGPYNLRYRVWADW 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 VAAFL-----GDHAASHLVYGDVVMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 LAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 VHSGPDDGPYDAMNRGV-----GVATGEWVLFLGADD-----TLYEPTTLAQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity es 47; Conserv
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
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SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                   TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                    APPLICANT: Gotschlich, Emil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLYSYLICAYNYEKYFAQSLAAVVNQTWRNLDILIYDDGSTDGTLAIAKDFQKRDSRIKI 62
                                                                                                                              CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                         COUNTRY: USA
ZIP: 07601
                                                                                                                                                                      STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 03-Dec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/312,387 FILING DATE: July 7, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/333,412 FILING DATE: 15-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/007, 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 348 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                              DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                          INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 343-1684
                                                                                                                                                                                              Klauber & Jackson
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                                                                                                                                                                                                                                                      OLIGOSACCHARIDES, AND GENES ENCODING THEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; DB 12;
. 8.9e-09;
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                                                                                                CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                             PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-05
                                                                                                                                                                                       FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                         TITLE OF INVENTION: Identification of Essential Genes
                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Haselbeck, Robert
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Ohlsen, Kari Zyskind, Judi

Judith W.

Xu, H. Howard Carr, Grant J.
Yamamoto, Robert T. Trawick, John D. Wall, Danie

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CATION NUMBER:

60/207,727 60/206,848

2000-05-26 2000-05-23

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US-09-815-242-4950
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                   Sequence 4950, Application Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                           179 VIDG----GLRYDTERDW 192
                                                                                                                                                                                                                                                   123 MGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAF --- FPFGNPIHNNTMIMRRS 178
                                                                                                                                                                                                                                                                                                      106
                                                                                                                                                                                                       158 LFDGIGPYNLRYRVWADW 175
                                                                                                                                                                                                                                                                                                                                             63 LAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 122
                                                                                                                                                                                                                                                                                                                                                                                           64 VHSGPDDGPYDAMNRGV-----GVATGEWVLFLGADD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 PVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/007,267
FILING DATE: 03-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/312,387 FILING DATE: July 7, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 VAAFL-----GDHAASHLVYGDVVMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         PLVSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRIKI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/333,412 FILING DATE: 15-Jun-1999
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                                      Application US/09815242
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23.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 158; DB 12;
Pred. No. 8.9e-09;
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LENGTH: 706
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Best Local Similarity
                                                          PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/815, CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: ELITRA.011A
                      NUMBER OF SEQ
                                          PRIOR FILING DATE:
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                                                                                                                            PRIOR FILING DATE: 2000-11-
                                                                                                                                                                    RIOR FILING DATE: 2000-10-23
                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                             RIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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                                                                                                                                                                                                                                                                            RIOR APPLICATION NUMBER: 60/206,848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354 QDYDLVLR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 ADWDFNIRCFSNPALITRYMDVVISEYNDMTGFSMRQGTDKEFRKRLP--MYFW 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 DLIYSDEDKIDMDGNRSDPAFKPDWSPDLLLGTNYISHLGVYRRSILEEIGGFRKGYEGS 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 RVVFREQNGHISEATNSALAIATGEFVALLDNDDELAINAFYE-----VVKVLNENPEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 VYHSGPDDGPY-DAMNRGVGVATGEWVLFLGADDTL----YEPTTLAQVAAFLGDHAAS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 PVFSIIIPTFNAAVT-LQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRL
                                                                                                                                                                                                             APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-05-26
                                                                                                                                              APPLICATION NUMBER: 60/253,625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
FastSEQ
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Zyskind, Judith W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wall, Daniel
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for Windows Version
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26.1%;
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                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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SEQ ID NO 39
LENGTH: 270
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TITLE OF INVENTION: Campylobacter Glycosyltransferases
TITLE OF INVENTION: Gangliosides and Ganglioside Mimic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/118,213 PRIOR FILING DATE: 1999-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/816,028A CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gilbert, Michel
APPLICANT: Wakarchuk, War
APPLICANT: National Resea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 PKISIAMPYYNVEEKWLRLCIDSILNQVYTNWELCMADDASTDPNVKKILTEYQQLDERI 241
162
                                      183 SNPALITRYMDVVISEYNDMTGFSMRQGTDKEFRKRLPMYFW----VAGWETC 231
                                                                              118 AFVHRVKTKQFYRFKQD----
                                                                                                                       123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 ADWDFNIRCFSNPALITRYMDVVISEYNDMTGFSMRQGTDKEFRKRLP--MYFW 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 DLIYSDEDKIDMDGNRSDPAFKPDWSPDLLLGTNYISHLGVYRRSILEEIGGFRKGYEGS
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                                                                                                                                                                                                                                                                                                                              Local Similarity 23.
les 54; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 PVFSIIIPTFNAAVT-LQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRL 62
                                                                                                                                                                                                                                                                                     4 PVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 09/495,406 FILING DATE: 2000-01-31
                                                                                                                                                           IFQNEENLGTFASRNLGVLHSSSDFIMFLDSDDFL---TPDACEIAFKEMKKGFDLLCFD
                                                                                                                                                                                                  VHSGPDD-GPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYGD 122
                                                                                                                                                                                                                                            PQLSITIPLENSCDFISRALQSCINQTLKDIEILIIDDKSKDNSLNMYLEFAKK-DPRIK 60
KKDIILKSFEKIKIDE----
                                                                                                                   VVMRSTKSRHAGPEDLDRLLFETNLCHQSIFYRRELFDGIGPYNLRYRVWADWDFNIRCF
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26.1%;
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RLNYGEDVLF - - - CYTYFMFCEKIAVFKTC
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Pred. No. 9.1e-09;
8; Mismatches 96;
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Pred. No. 2.7e-08;
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                                                                              -EVFNQKEFLEFLS--KQRHFCWSVW---AKCF
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US-09-767-041-52

Sequence 52, Application US/09767041

Patent No. US/0020055188A1

GENERAL INFORMATION:

APPLICANT: SMITH, Hilda

TITLE OF INVENTION:

APPLICANTION WINDER: US/09/767,041

PRIOR APPLICATION WUNDER: US/09/767,041

CURRENT PAPPLICATION WUNDER: PCT/NL99/00460

PRIOR APPLICATION WUNDER: EP98202465.5

PRIOR APPLICATION WUNDER: EP98202467.1

PRIOR APPLIC
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Sequence
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4, Appli 2, Appli 2, Appli 4067, Ap 168, App 9, Appli 4, Appli 10, Appl

Sequence Sequence

5, Appli 5, Appli 12, Appli 5, Appli 4051, Ap 198, App 202, App 5633, Ap

Sequence Sequence Sequence

5, Appli

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Post-processing: Minimum Match 0%
Maximum Match 10
Listing first 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein search, using sw model
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1
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Match
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                          262574 seqs, 29422922 residues
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/ACTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/Dackfiles1.pep:*
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US-08-746-682A-10
US-08-312-387B-11
US-08-683-426-3
US-08-683-426-3
US-08-683-426-11
US-08-683-458-13
US-08-683-458-13
US-08-683-458-13
US-08-683-458-13
US-08-478-140B-3
US-08-478-140B-3
US-09-333-412-11
US-09-333-412-11
US-09-338-943-3
US-09-338-943-3
US-09-338-943-3
US-09-38-943-277-3
US-09-437-277-3
US-09-437-277-3
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      Sequence 10, Appl Sequence 3, Appli Sequence 3, Appli Sequence 11, Appli Sequence 3, Appli Sequence 3, Appli Sequence 11, Appli Sequence 11, Appli Sequence 3, Appli Sequence 3, Appli Sequence 11, Appli Sequence 11, Appli Sequence 15, Appli Sequence 15, Appli Sequence 17, Appli Sequence 5, Appli Sequence 12, 
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US-08-597-236-10
                                                                                                                                                       Matches
                                                                                                                                                                             Query Match
Best Local :
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 3025
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 426
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95201669.9
FILING DATE: 20-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: FARUCCI A., Allan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/597,236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: STINGELE, Fr
APPLICANT: MOLLET, Beat
TITLE OF INVENTION: LAC'
TITLE OF INVENTION: EXOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
65 HSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYG
                                                                                                                                                     Local Similarity
nes 42; Conserv
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                                                                                                 5 VFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLVV 64
                                                        LISIVIPVYNVEKYLEKCLOSVONOTYNNFEVILVNDGSTDSSLSICEKFVNO-DKRFSV 64
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115.5
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5. 5733765
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US-08-878-360-12
US-08-478-140B-5
US-09-333-412-12
US-09-333-412-12
US-09-333-412-12
US-09-334-001C-4051
US-08-961-083-202
US-09-134-001C-5633
US-08-270-581-2
US-09-134-001C-4067
US-08-961-083-168
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US-08-960-048-9
US-08-961-083-168
US-08-961-083-168
US-08-960-048-9
US-08-961-083-168
US-08-961-083-168
US-08-961-083-168
US-08-961-083-168
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Pred. No. 2e-10;
                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                       Sequence 3, Application US/08312387B Patent No. 5545553
                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                      CORRESPONDENCE ADDRESS:
                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                        PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: CFILING DATE: 20-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 14-NOV
                                                                                                                                                                                                                                                                               65 FSKENGGMSSARNFGIKKAKGSFITFVDSDDYI---
                                                                                                                                                                                                                                                                                                                  65 HSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0,
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                                    STREET:
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                       CITY:
                                                      ADDRESSEE:
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                   Hackensack
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                                                                                                   Gotschlich, Emil C.
VENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
VENTION: OLIGOSACCHARIDES, AND GENES ENCODING THE
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Pred. No.
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Best Local Similarity 23.7%;
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                      CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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OPERATING SYSTEM:
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REFERENCE/DOCKET NUMBER: 600
                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
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                  APPLICATION NUMBER: FILING DATE: July
                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 LAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 122
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   CLASSIFICATION:
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N: 435
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                July 7, 1994
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                                                                                                                                                                                                                                                                                                 OLIGOSACCHARIDES,
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                                                                      Release #1.0,
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Pred. No. 4.9e-10;
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                                                                      Version #1.25
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                    CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: Septembe
                                                                                                                                                                                                                                       SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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LENGTH: 348 amino acic
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                                 TELECOMMUNICATION INFORMATION:
                                                                                                   CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
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                                                 NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
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September 26, 1994
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23.7%;
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Pred. No. 4.9e-10;
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Best Local Similarity
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Sequence 11, APF-
Sequence 11, APF-
Sequence 11, APF-
No. 5705367
                                           TELEX: 133521
INFORMATION FOR SEQ ID NO:
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SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein
                             SEQUENCE CHARACTERISTICS
                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 MGAWLEYLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAF----FPFGNPIHNNTMIMRRS 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITLE OF INVENTION:
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                                                                           TELEFAX:
                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
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                                                                                                                                NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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amino acid
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SYSTEM: PC-DOS/MS-DOS
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GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
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Pred. No. 4.9e-10;
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JS-08-683-426-11

MOLECULE TYPE:

protein

TOPOLOGY:

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Best Local 9
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                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/312.
FILING DATE: September 26,
                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acid
                                                                                                                                                                                                                                           TELEPHONE: 201 487-5800
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release
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                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                       NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
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                                                                                                                                                       TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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                                                Local Similarity es 47; Conserv
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                                                Conservative
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ber 26, 1994
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                                           Score 158; DB 1;
Pred. No. 4.9e-10;
7; Mismatches 80;
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Best Local Similarity
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APPLICANT: Gotsch
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPAX: 201 343-1684
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CURRENT APPLICATION DATA
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   106 VAAFL-
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NAME: Jackson Esg., David A.

REGISTRATION NUMBER: 26,742

REGISTRATION NUMBER: 600-1-095A
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IBM PC compatible
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-GDHAASHLVYGDVVMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRE 157
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In Release #1.0, Version #1.25
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GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
OLIGOSACCHARIDES, AND GENES ENCODING THE
                                                                                                                                                                                     11.3%; Score 158; DB 1; 23.7%; Pred. No. 4.9e-10;
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ber 26, 1994
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RESULT 9 US-08-878-360-3

Sequence 3, Application US/08878360 Patent No. 5945322

GENERAL INFORMATION:

Gotschlich,

Emil C.

TITLE OF INVENTION: NUMBER OF SEQUENCES: 1

ADDRESSEE

CURRENT APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

08/683,426

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COUNTRY:

USA

New Jersey

411 Hackensack Avenue

Klauber & Jackson

07601

APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REPERENCE/DOCKET NUMBER: 600-1-095B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                              123 MGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAF----FPFGNPIHNNTMIMRRS 178
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                                                                                                                                                                                64 VHSGPDDGPYDAMNRGV-----GVATGEWVLFLGADD-----
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                                                                                                                                           63 LAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 122
                                                                                                                                                                                                                                                                4 PVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLV 63
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                                                                                                      ----GDHAASHLVYGDVVMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRE 157
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                                                                                                                                                                                                                                                                                                       Score 158; DB 2;
Pred. No. 4.9e-10;
7; Mismatches 80;
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Best Local Similarity
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RESULT 11
US-08-478-140B-3
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US-08-878-360-11
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LENGTH: 348 amino acids
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NAME: Jackson Esq., Davi
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CORRESPONDENCE ADDRESS:
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                                                                               VIDG----GLRYDTERDW
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106 VAAFL---

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158 LFDGIGPYNLRYRVWADW 175

; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-878-360-3

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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

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TELEFAX:

201 343-1684

LENGTH:

amino acid

348 amino acids

Matches

Conservative

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Query Match
Best Local Similarity

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                                                                               Sequence 8, Application US/08478140B Patent No. 6127153
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Best Local Similarity
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                                                                GENERAL INFORMATION:
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   TITLE OF INVENTION:
                                 APPLICANT:
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MEDIUM TYPE: Floppy disk
                    APPLICANT:
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                                                                                                                                                                                                                                                                                                          63 LAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 122
                                                                                                                                                                                                                                                                                                                                          64 VHSGPDDGPYDAMNRGV-----GVATGEWVLFLGADD-----
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NAME: Laura A. Coruzzi
REGISTRATION NUMBER: 30,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
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                                                                                                                                                                               VIDG----GLRYDTERDW
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BUCZALA, STEPHANIE L.

TENTION: METHOD OF TRANSFERRING AT LEAST TWO
                                ROTH, STEPHEN
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                                                JOHNSON, KARL F.
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SYSTEM: PC-DOS/MS-DOS
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METHOD OF TRANSFERRING AT LEAST TWO SACCHARIDE UNITS WITH A POLYGLYCOSY.
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23.7%; Pred. No. 4
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CORRESPONDENCE ADDRESS:

STREET: 411 Hackensack Avenue

Hackensack

ADDRESSEE: Klauber & Jackson

TITLE OF INVENTION: NUMBER OF SEQUENCES:

OLIGOSACCHARIDES,

Emil C

GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS

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                                                                                          RESULT 13
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Sequence 3, Application US/093
Patent No. 6342382
GENERAL INFORMATION:
GENERAL SECTION:
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Laura A. Coruzzi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                             179 VIDG----GLRYDTERDW
                                                                                                                                                                             158 LFDGIGPYNLRYRVWADW 175
                                                                                                                                                                                                                123 MGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAF----FPFGNPIHNNTMIMRRS 178
                                                                                                                                                                                                                                               106 VAAFL-----GDHAASHLVYGDVVMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRE 157
                                                                                                                                                                                                                                                                                    63 LAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 122
                                                                                                                                                                                                                                                                                                                       64 VHSGPDDGPYDAMNRGV-----GVATGEWVLFLGADD-----TLYEPTTLAQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 23.7 tes 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: F
SOFTWARE: PatentIn
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                                                                                                                                                                                                                                                                                                                                                                                           4 PVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLV 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                     Application US/09333412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 amino acids
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                              11.3%; Score 158; DB 3; 23.7%; Pred. No. 4.9e-10; tive 37; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SACCHARIDE UNITS WITH A POLYGLYCOSYLTRANSFERASE, POLYGLYCOSYLTRANSFERASE AND GENE ENCODING A
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                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/09333412
Patent No. 6342382
GENERAL INFORMATION:
GENERAL APPLICANT: Gotschlich, Emil C.
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 VIDG----GLRYDTERDW 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 LFDGIGPYNLRYRVWADW 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 MGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAF----FPFGNPIHNNTMIMRRS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 VAAFL-----GDHAASHLVYGDVVMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 LAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 122
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              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US/09/333,412
APPLICATION 15-Jun-1999
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
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                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VHSGPDDGPYDAMNRGV------GVATGEWVLFLGADD------TLYEPTTLAQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLVSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRIKI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity 47; Conserv
                                                                                                                         COUNTRY: USA
                                                                                                                                          STATE: New Jersey
                                                                                                                                                             CITY: Hackensack
                                                                                                                                                                                     STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/312,387 FILING DATE: July 7, 1994
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  SOFTWARE:
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PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                 GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF OLIGOSACCHARIDES, AND GENES ENCODING THE
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US-09-338-943-3
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 VAAFL-----GDHAASHLVYGDVVMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRE 157
                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 LAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 VHSGPDDGPYDAMNRGV-----GVATGEWVLFLGADD-----TLYEPTTLAQ 105
                                                                                                                                                                 STATE:
                                                                                                                                                                                    CITY: New York
                                                                                                                                                                                                     STREET:
                                                                                                                        COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 PVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09338943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 348 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/312,387 FILING DATE: July 7, 1994
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                                                                                                                                                              New York
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                                                                                                                                                                                                     1155 Avenue
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                   PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                          JOHNSON, KARL F.
                                                                                                                                                                                                                        Pennie &
                                                                                                                                                                                                                                                                                                                                                                                         STEPHEN
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METHOD OF TRANSFERRING AT LEAST TWO
SACCHARLDE UNITS WITH A POLYCLYCOSYLTRANSI
POLYGLYCOSYLTRANSFERASE AND GENE ENCODING
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                                                                                                                                                                                                       of.
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                                                                                                                                                                                                                                                                                                                         POLYGLYCOSYLTRANSFERASE,
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TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8866
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-338-943-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Laura A. Coruzzi
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7188-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,140
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ATTORNEY/AGENT INFORMATION:
                                                                                   179 VIDG----GLRYDTERDW 192
                                          158 LFDGIGPYNLRYRVWADW 175
                                                                                                                                  106 VAAFL-----GDHAASHLVYGDVVMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRE 157
                                                                                                                                                                                                                        64 VHSGPDDGPYDAMNRGV-----GVATGEWVLFLGADD------TLYEPTTLAQ 105
                                                                                                                                                                                63 LAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA: 122
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Search completed: April 17, 2003, 17:29:27 Job time : 30 secs

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Result
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13.1	13.1	13.3	13.3	13.3	13.3		13.4		13.5			13.7		14.0	14.3		14.6	14.7		14.8			16.5	16.6	17.0	17.0	17.6	17.7
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## 088109; 01-NOV-1998 (TrEMBLrel. 08, (TrEMBLrel. 08, (TrEMBLrel. 17, PRELIMINARY; 266 A

ALIGNMENTS

Created)
Last sequence up

update) update)

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; MCBI\_TaxID=44282, 1770, 1764; Mycobacterium paratuberculosis, Mycobacterium avium. GSD OR GTFD. Mycobacterium avium subsp. silvaticum, protein. and

Mycobacterium.

01-JUN-2001

SEQUENCE FROM N.A. .paratuberculosis;
Martin H., Ford J

SPECIES=M.avium subsp. silvaticum, and M.paratuberculos: Tizard M., Bull T., Millar D., Doran T., Martin H., Ford Hermon-Taylor J.;
"A low G+C content element in Mycobacterium avium subsp. paratuberculosis and M. avium subsp. silvaticum with hom in M. tuberculosis."; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases homologous genes

SEQUENCE FROM N.A.

SPECIES-M.avium; STRAIN-2151; Eckstein T.M., Lambert M.L., Brennan P.J., Belisle J.T., Inamine J.M.; "Identification of a gene cluster involved in glycopeptidolipid biosynthesis and of a gene cluster encoding daunorubicin resistance in two strains of Mycobacterium avium serovar 2."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

SEQUENCE FROM N.A.

SPECIES-M.avium; STRAIN-TMC 724;

Eckstein T.M., Brennan P.J., Inamine J.M., Belisle J.T.; "Identification of gene cluster involved in glycopeptidolipid biosynthesis and of a gene cluster encoding daumorubicin resistwo strains of Mycobacterium avium serovar 2."; resistance

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SEQUENCE FROM N.A.
Wang L., Reeves P.R.;
"The E. coli Olli and S. enterica 035
"The E. coli olliose containing
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
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EMBL; AJ22
EMBL; AJ22
                                                                                                                                                Submitted (JUL-2000) to the EMBL/GenBank/DDBJ EMBL; AF285969; AAK83018.1; -. InterPro; IPR001173; Glycos_transf_2. pfam; PF00535; Glycos_transf_2; 1.
                                                                                                                                                                                                                                                                                            Salmonella enterica.
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L; AJ223832; CAA11574.1; -.
L; AJ223833; CAA11578.1; -.
L; AF143772; AAD44222.1; -.
L; AF125999; AAD20376.1; -.
erPro; IPR001173; Glycos_transf_2.
m; PF00535; Glycos_transf_2; 1.
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IVSEKDRGIYDAWNKAVDLSSGDWIAFIGSDDVYYHTDAITSLVKGAAISNGAPVVYG--
                     VHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYGDV 123
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266; Conserv
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72; Conserv
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                                                                                   Score 298.5; DB 2;
Pred. No. 4.2e-18;
Pred. No. 4.2e-18;
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Pred. No. 1.2e-114;
); Mismatches 0;
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01-MAY-2000 (TrEMBLrel. 13, La
01-JUN-2001 (TrEMBLrel. 17, La
Putative glycosyl transferase.
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"Sequencing of Escherichia coli Oll1 Oantigen
identification of Oll1-specific genes.";
J. Clin. Microbiol. 36:3182-3187(1998).
EMBL; AF078736; AAD46731.1; -
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MEDLINE-98449835; PubMed-9774562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96060831; PubMed=7590310; Bastin D.A., Reeves P.R.;
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Pfam; PF00535; Glycos_transf_2; 1.
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Pred. No. 4.7e-18;
2; Mismatches 86
                                                                                                   SFIVRKKNNISCLNIQLI
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Hypothetical
SEQUENCE 26
                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Cr. 01-JUN-2001 (TrEMBLrel. 17, La. 01-MAR-2002 (TrEMBLrel. 20, La. Hypothetical 31.4 kDa protein.
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01-MAR-2002 (TrEMBLrel. 20, La
01-JUN-2002 (TrEMBLrel. 21, La
Hypothetical 31.4 kDa protein.
                                                                                                                                                      and transfer genes of the lipopolysaccharide-related Leptospira interrogans serovar Copenhageni.";
J. Bacteriol. 179:1262-1267(1997).
                                                                                                                                                                                                            MEDLINE-97175555; PubMed-9023210; Mitchison M., Bulach D.M., Vinh T
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Bacteria; Spirochaetales; Leptospiraceae; Leptospira
             SEQUENCE FROM N.A. STRAIN-AKIYAMI A;
                                                     de la Pena-Moctezuma A., Bulach D.M., Adler B.; 
"Genetic differences among the LPS biosynthetic loci of 
Leptospira interrogans and Leptospira borgpetersenii."; 
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                              STRAIN-L45;
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                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                Bacteria; Spirochaetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           de la Pena-Moctezuma A., Bulach D.M., Adler B.; "Genetic differences among the LPS biosynthetic loci Leptospira interrogans and Leptospira borgpetersenii. EPTMS Immunol. Med. Microbiol. 31:73-81(2001).
                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   NCBI_TaxID=173;
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MEDLINE-21369626; PubMed=11476985;
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                                                                                                                                                                                                                                                                                                             Septospira interrogans
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                                                                                                                                                                                             Identification and characterization of the dTDP-rhamnose
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265 AA; 3
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 PubMed=11476985
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"Genetic differences among the LPS biosynthetic loci of
Leptospira interrogans and Leptospira borgpetersenii.";
FEMS Immunol. Med. Microbiol. 31:73-81(2001).

EMBL; AF316500; AAL49428.1; -.
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein.

SEQUENCE 265 AA; 31438 MW; DACE187B481AF700 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leptospira interrogans and Leptospira FEMS Immunol. Med. Microbiol. 31:73-8 EMBL; U61226; AAK19913.1; -- EMBL; AF316557; AAK49948.1; -- Interpro; IPR001173; Glycos_transf_2. Pfam; PF00535; Glycos_transf_2; 1.
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01-MAR-2002 (TrEMBLrel 20, La
01-JUN-2002 (TrEMBLrel 21, La
Hypothetical 31.4 kDa protein.
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"Genetic differences among
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                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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uma A., Bulach D.M.,
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                                                            de la Pena-Moctezuma A., Bulach D.M., Adler B.; "Genetic differences among the LFS biosynthetic loci Leptospira interrogans and Leptospira borgpetersenii. FEMS Immunol, Med. Microbiol. 31:73-81(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        de la Pena-Moctezuma A., Bulach D.M., Adler B.; "Genetic differences among the LFS biosynthetic loci Leptospira intercogans and Leptospira borgpetersenii. FEMS Immunol. Med. Microbiol. 31:73-81(2001). EMBL, AF316564; AAL4962.1; "...
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MEDLINE=21369626; PubMed=11476985;
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InterPro; IPR001173; Glycos_transf_2;
Pfam; PF00535; Glycos_transf_2; 1.
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Interpro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    de la Pena-Moctezuma A., Bulach D.M., Adler B.;
"Genetic differences among the LPS biosynthetic loci
Leptospira interrogans and Leptospira borgpetersenii.
FEMS Immunol. Med. Microbiol. 31:73-81(2001).
EMBL; AF316563; AAL49460.1; ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF316562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-SALINEM, BALLICO, SWART, AN MEDLINE-21369626; PubMed-11476985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leptospira interrogans. Bacteria; Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Hypothetical 31.4 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8VL41;
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                                                                                                                                                                                                                                                                                                                      4 PVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTD-----RTLDIANSFRP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MTA--PVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTD-----RTLDIA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTAKEPKISIITINLNNLEGLRKTLESVKSQTYTNFELIVVDGGSTDGSFEYLKSNLDLI
                                                                               ADWDFNIRCFSNPALITRYMDVVISEYNDMTGFSM----RQGTDKEFRKRLPMYF
                                                                                                                                                             HLVYGDVVMRSTKSRHAGPEDLDRLLE----ETNLCHQSIFYRRELEDGIGPYNLRYRVW
                                                                                                                                                                                                                                                                                   PKISITTINLNNLEGLRKTLESVKSQTYTNFELIVVDGGSTDGSFEYLKSNLDLIKKFIS
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                                         ADFEFFHRFWFNKNIKIKHASVFVTLY-DFNGVSAQPKNRKRIAEEYQKIKKKYF
                                                                                                                       DLVYGNILIDSKUNGIIERKYPDRLNYFYWSIKSLCHQAVFIRKSLFDLYGYYNEEYLFA
                                                                                                                                                                                                                                      ELGSRLVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAAS 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF316556;
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                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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265 AA;
                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAL49446.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAL49450.1;
                                                                                                                                                                                                     KDKGIYNAQNKGILLSKGEYLVFLNAGDTLLQKNILLEISKFLDQDV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                31422 MW;
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                                                                                                                                                                                                                                                                                                                                                          Score 271; Db .,
Pred. No. 9.3e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 274; DB 2;
Pred. No. 5.1e-16;
0; Mismatches 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                E5539162FA877A9D CRC64;
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Best Local
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248 AA;
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                                                                                                                                                               de la Pena-Moctezuma A., Bulach D.M., Adler B.; "Genetic differences among the LPS biosynthetic loci of Leptospira interrogans and Leptospira borgpetersenii."; FEMS Immunol. Med. Microbiol. 31:73-81(2001).
                                                                                                                                                                                                                                                                                                                                                                                      Leptospira interrogans.
Bacteria: Spirochaetales; Leptospiraceae; Leptospira
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation updat
Hypothetical 31.4 kDa protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9EXY1;
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                                                                        Pfam; PF0053
Hypothetical
                                                                                                                                           FEMS Immunol. Med. Microbiol. EMBL; AF316561; AAL49456.1; -.
                                                                                                                                                                                                                                                                                                 STRAIN-MWOGOLO;
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OBVIW8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-M1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli
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                                                                                                                       InterPro; IPR001173; Glycos_transf_2.
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                                                                                                                                                                                                                                                                   MEDLINE-21369626; PubMed-11476985;
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|crobiology 147:599-610(2001).
|ABL; AX012190; AAG41755.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLV-VH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SESDNGIYDALNKGINLSTGDIIGFVHSDDLLARPDIIETIVSRFHETKAD-VVYGDLVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEKNQIDIIKRYWRSGPFKRSKLSLGWAPPHPSFYMRRELYKDDGYFDLSYRIAADYDOM 178
                                                                                       PF00535; Glycos_transf_2;
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                                                    265 AA;
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                                                    31442 MW;
    19.18;
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Pred. No. 1.
    Score 267
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                                               A39258BFA6388DAA CRC64;
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nes 77;
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RESULT 12
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                                                                                                                                                                                                                                                                  EMBL; AY012189; AAG41752.1; -
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
                                                                                                                                                                                                                                            Transferase.
SEQUENCE 2
                                                                                                                                                                                                                                                                                                     in Salmonella enterica.";
Microbiology 147:599-610(2001).
                                                                                                                                                                                                                                                                                                                              Jensen S.O., Reeves P.R.; "Molecular evolution of the GDP-mannose
                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
Bacteria; Proteobacteria;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21135136; PubMed=11238967;
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                                                                                                            SGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYGDVVM
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VRVLKRDDIKVSYVPQV
                        IRCFSNPALITRYMDVV
                                                                       RS-----TKSRHAGPFDLDRLLFETNLCHQSIFYRRELFDGIGPYNLRYRVWADWDFN
                                                                                               SESDKGIYDALNKGINLSTGDIIGFVHSDDVLARPDIIETIVGRFHETKAD-VVYGDLVF
                                                                                                                                              SIITVTYNSEKTLRNTLESIELQTYSDIEYIIIDGGSTDNTLKIIN----EVSTRVTRCL 59
                                                FEKNQIDIIKRYWRSGPFKRSKLSLGWAPPHPSFYMRRELYKDDGYFDLSYRIAADYDQM
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                                                                                                                                                                                             1 Similarity
67; Conserv
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Last annotation updat
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                                                                                                                                                                                                         Score 266.5;
Pred. No. 2.
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ches 93;
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RESULT 13 Q9ZGK3

Q9ZGK3

PRELIMINARY;

PRT;

251

3

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RESULT
Q9EXZ1
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Best Local S
Matches 67
Query Match
Best Local S
Matches 74
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01-MAR-2001 (TrEMBLrel. 16, L;
01-DEC-2001 (TrEMBLrel. 19, L;
01-DEC-2001 (TrEMBLrel. 19, L;
Putative glycosyl transferase
Salmonella enterica subsp. en
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 29.0 kDa protein.
Leptospira borgpetersenii.
Bacteria; Spirochaetales; Leptospiraceae; Leptospira
                                                                                                                            in Salmonella enterica.";
Microbiology 147:599-610(2001).
EMBL; AY012186; AR641745.1; -.
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
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EMBL; AF078135; AAD12966.1; -
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00335; Glycos_transf_2; 1.
                                                                                                                Transferase
                                                                                                                                                                                                                                                                                                                        STRAIN-M264;
                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision;
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                                                                                                                                                                                                                                                                                                 MEDLINE-21135136; PubMed-11238967;
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                                                                                                                                                                                                                                                    Molecular evolution of the GDP-mannose
                                                                                                                                                                                                                                                                                                                                             EQUENCE FROM N.A.
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67; Conserv
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    Similarity 28.
74; Conservative
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29.1%;
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                                                                                           29275
                                                                                           MW.
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Score 255; DB
Pred. No. 2.2e
52; Mismatches
    52;
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Last annotation update)
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  es 89;
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                                          DB 2;
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iobovis.";
                                            Length 254;
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  48;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 De la Pena-Moctezuma A., Bulach D.M.,
Submitted (APR-1999) to the EMBL/GenB
EMBL; AF144879; AAD52183.1; -.
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
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Bacteria; Spirochaetales; Leptospiraceae;
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EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 254.5; DB 2
Pred. No. 2.6e-14;
8; Mismatches 94
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                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III. Tekaia F.,
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Bornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from t
Complete genome sequence.";
Nature 30:1527-24/10008
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                                                             Peterson J., DeBoy R., Dodson R., Kolonay J.F., Nelson W.C., Umayam Delcher A., Utterback T., Weidman
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Holland D., Wolk C.P.;
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cyanobacterium Anabaena sp DNA Res. 8:205-213(2001).

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Yasuda M., Tabata S.;
"Complete genomic sequence Nakazaki N., Shimpo

Watanabe A., Iriguchi M., Ishikav Kishida Y., Kohara M., Matsumoto

Kaneko T.,

Nakamura

Kuritz

itz T., Sasamoto S., Kawashima K., Kimura T.

Matsuno A.,

Muraki A.,

Takazawa

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mura Y., Wolk C.P., Kurit
lguchi M., Ishikawa A., K
ara M., Matsumoto M., Mat
mpo S., Sugimoto M., Tak
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36; Mismatches
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STRAIN=K12 / MG1655;

K MEDLINE=94316500; PubMed=8041620;
K MEDLINE=94316500; PubMed=8041620;
A Sofia H.J., Burland V., Daniels D.L., Plunket
A Sofia H.J., Burland V., Daniels D.L., Plunket
T "Analysis of the Escherichia coli genome. V.
Tregion from 76.0 to 81.5 minutes.";
region from 76.0 to 81.5 minutes.";
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16-OCT-2001 (Rel. 4
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              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                  MEDLINE-89174812; PubMed-2647748; Aronson B.D., Somerville R.L., Epperly B.R., Dekker E.E.; "The primary structure of Escherichia coli L-threonine
                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Escherichia.
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                                                                                                                       dehydrogenase.
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                                                                                      3101. Chem. 264:5226-5232(1989).
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
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Q57022; P96336;
15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
15-JUN-2002 (Rel. 4
EMBL; U32768; HSSP; P39621; TIGR; HI0868;
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SEQUENCE
                                                                                                                                                                                                           Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F. Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M. McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C. Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                           use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
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Haemophilus
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InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
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PIR; B33276; B33276
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                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                               Science 269:496-512(1995).
-i- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY
                                                                                                                                                                                                                                                                                                         STRAIN=Rd / KWZU / ATCC 31301,
MEDLINE-95350630; PubMed-7542800;
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                                                 or send an email to license@isb-sib.ch)
                                                                                                the European
                                                                                                                                                                                     "Whole-genome
                                                                                                                                                                                                   Venter J.
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X06690; CAA29885.1;
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15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
15-JUN-2002 (Rel. 4
                                                                                                                                                                                                                                                                                                                              Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick C. McKenney K., Sutton G., Fitzhugh W., Fields.A., Googyne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Secott J.D., Shirley R., Liu E.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D. Utterback T.R., Hanna M.C., Nguyen D.T., Sandek D.M., Brandon R.
                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                              Fine L.D., Fritchman J.L.,
Gnehm C.L., McDonald L.A.,
Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., Whi
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=Rd / KW20 /
                          Hypothetical protein;
                                                                        TIGR; HI1578;
                                                                                   EMBL; U32832; AAC23227.1;
                                                                                                                   or send
                                                                                                                                                                                                                                                   Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
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                                        InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
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7CBC2681039AB5B4 CRC64;

EMBL; U38473; AAC77840.1; EMBL; AE000295; AAC75116.1;
EcoGene; EG13573; wcaE.

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Best Local
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STRAIN=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., RC
Riley M., Davis N.W., Kirkpatrick H.A., Goe
                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                  This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                     STRAIN-K12;
Reeves P.R.;
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Stevenson G., Andrianopous.
Torganization of the Escherichia coli K-12 gene usual polysaccharide colanic for production of the extracellular polysaccharide colanic Racteriol. 178:4885-4893(1996).
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01-NOV-1997 (Rel. 35, Last seq
16-CCT-2001 (Rel. 40, Last ann)
Putative colanic acid biosynth
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                                                                                                                                                                                                                                                                                                          Submitted
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                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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                                                                                                                                                        InterPro; IPR001296; Glycos_transf_1: InterPro; IPR001173; Glycos_transf_2: Pfam; PF00534; Glycos_transf_1; 1. Pfam; PF00535; Glycos_transf_2; 2.
                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                multicellular development.";
J. Bacteriol. 178:1631-1639(1996).
-1- FUNCTION: INVOLVED IN O-ANTIGEN BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; delta subdivision; Myxobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
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01-NOV-1997
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01-NOV-1997
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                                                                                                                                                                                                                                                                       EMBL; U36795; AAB05019.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guo D., Bowden M.G., Pershad R., Kaplan H.B.; "The Myxococcus xanthus rfbABC operon encodes an ATP-binding transporter homolog required for O-antigen biosynthesis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96198166; PubMed=8626291;
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                                                                                                         Lipopolysaccharide biosynthesis.
SEQUENCE 1275 AA; 139596 MW;
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     Local Similarity 30.1
les 58; Conservative
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(Rel. 35, Last sequence update)
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                           Score 146.5;
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Best Local
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Pfam; PF00535; Glycoz, Transf. 2; 1.
EXOPOLYSACCHARIDE Synthesis; Transferase; Glycos
SROUENCE 301 AA; 34788 MW; 99D0EE3080E6EC06
                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                            synthesis of Erwinia amylovora."
Mol. Microbiol. 15:917-933(1995)
-!- FUNCTION: INVOLVED IN THE BI
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Q46632;
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                                                                                                                                                                                                                                   EMBL; X77921; CAA54883.1; -.
InterPro; IPR001173; Glycos_transf_2.
                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bugert P., Geider K.;
"Molecular analysis of the ams operon required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Erwinia amylovora.
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15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95319333;
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PATHWAY: Exopolysaccharide biosynthesis.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
YEPTTLAQVAAFL:
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                                                                                                                 FSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTD--RTLDIANSFR-PELGSRL
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Bourliet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningstein G., Kroph S., Kumano M.,
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RA Kobayashi Y., Kepilus A., Lardinois S., Lauber J., Lazarevic V.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle D., Rapoport G., Rey.M., Reynolds S.,
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Hullo M.F., Ionescu M., Lubochinsky B., Marceli
Presecan E., Santana M., Schneider E., Schweize
Rapoport G., Danchin A.;
"Bacillus subtilis genome project: cloning and
kb region from 325 degrees to 333 degrees.";
Mol. Microbiol. 10:371-384(1993).
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EMBL; 299123; CAB15824.1; -.
PIR; S39711; S39711.
SubtiList; BG10602; ywdF.
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
Complete proteome.
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SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
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                                                                              Bacteria; Proteobacteria;
                                                                                             Escherichia coli
                                               NCBI_TaxID=562;
                                                                Escherichia
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A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";

DNA Res. 3:137-155(1996).

Integral membrane protein (Potential).

SIMILARITY: TO Y. PESTIS HMS LOCUS PROTEIN HMSR AND TO S.EPIDERMIDIS ICAA.
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KENFRMW-----PLFFEYCLTTIWAFTCLVGF
                                                       DWDFNIRCFSNPALITRYMDVVISEYNDMTGF 205
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Pro; ITRO01173; Glycos_transf_2.
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hetical protein; Transmembrane;
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D90739; BAA35803.1; -.
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RESULT 13
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
succinoglycan biosynthesis protein exoU (EC 2
EXOU OR RB1071 OR SMB20948.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Bioinformat
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MEDLINE-94162682; PubMed-8118055;
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                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001173; Glycos_transf_2.
pfam; PF00535; Glycos_transf_2; 1.
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IIISAKNAADTIARAVASALAEP-EAAEVVVIDDGSTDDSASVARAADDGTGRLNVVRFE 69
                                                              IIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLVVHSG
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                                                                                                                                                                                                                                                              Complete proteome. 342 AA; 37017 N
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Pred. No. 6e-05;
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Becker A.,
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                                                                                                                                                      fixing endosymbiont Sinorhizobium meliloti.";

Proc. Natl. Acad. Sci. U.S.A. 98:989-9894(2001).

-I- FUNCTION: GLYCOSYLTRANSFERASE REQUIRED FOR THE SYNTHESIS OF SUCCINOGLYCAN (EPS 1). NEEDED FOR THE ADDITION OF THE FIFTH SUGAR (GLUCOSE), CATALYZES THE FORMATION OF A BETA-1,6 LINRAGE BETWEEN THE FOURTH AND FIFTH SUGAR.

-I- PAYHWAY: Exopolysaccharide biosynthesis.

-I- SUBCELLULAR LOCATION: Cytoplasmic.

-I- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Identification and analysis of the Rhizobium meliloti exoalinvolved in exopolysaccharide biosynthesis and mapping of plocated on the exoHKLAMONP fragment.";
Mol. Gen. Genet. 241:367-379(1993).
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                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21396508; PubMed-11481431;
Finan T.M., Weidner S., Wong K., Buhrmester J.,
Vorhoelter F.J., Hernandez-Lucas I., Becker A.,
Golding B., Puehler A.;
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MEDLINE=94067019; PubMed-8246891;
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Rhizobiaceae; Sinorhizobium.
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15-JUN-2002 (Rel. 41, Last sequence u)
15-JUN-2002 (Rel. 41, Last annotation
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                                                                                                                     CAUTION: Ref.1 sequence differs from frameshift in position 208.
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annotation update)
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Best Local S
Matches 69
                                                                                                                                                   EMBL; L20758; AAA16044.1; ALT_FRAME
EMBL; Z22636; CAA80347.1; -.
EMBL; AL603645; CAC49484.1; -.
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30-MAY-2000 (Rel.
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Pfam; PP00535; Glycos_transf_2; 1.

Transferase; Glycosyltransferase; Exopolysaccharide synthesis;
Plasmid; Complete proteome.
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PIR; S37029; S37029.
PIR; S39958; S39958.
                                 the European Bioinformatics Institute.
                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Electronic Control of the Electroni
                                                                                                                                                                                                                                                                         Regue M., Climent N., Abitiu N.,
Altarriba M., Tomas J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lipopolysaccharide (EC 2.-.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                  STRAIN=C3;
MEDLINE=21264367; PubMed=11371519;
MEDLINE=21264367; PubMed=11371519;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; 
Klebsiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klebsiella pneumoniae
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15-JUN-2002 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YNLRYRVWADWDF-----NIRCFSNPA--LITRYMDVVISEYNDMTGFSMRQGTDKEF
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69; Conserv
non-profit
and this st
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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Pred. No. 6.1e-
47; Mismatches
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, 6.1e-05;
\as 129;
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                                      restrictions
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                                                                                    a collaboration
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                                                                 outstation
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Best Local Similarity
Matches 47; Conserv
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Lipopolysaccharide biosynthesis; Transferase; Gl
SEQUENCE 258 AA; 29268 MW; D7458899030678D9
                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                   EMBL; AF146532; AAD37772.1;
                                                                                                                                                                                                                                                                                         InterPro;
154 LG 155
                       162
                                                 109
                                                                        102 TLAQVAAFLGDHAASHLVYGDVVMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRELFDG 161
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                                                                                                                                                 SVVMIAKNAADLLPDCLGSV---SWAD-EIIVLDSGSTDNTVELAR----RLGAQVYTHT
                       IG 163
                                                                                                                           GPDDGPYDAMNRGVGV-----ATGEWVLFLGADD-----
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                                                                                                                                                                                                   Conservative
                                                                                                  -WRGYGIQRQRAQDYATGDWVLMIDTDERVTPELRQAILKVLDAPQRGAIY
                                                                                                                                                                                                              9.4%;
                                                                                                                                                                                                   32;
                                                                                                                                                                                                              Score 131.5;
Pred. No. 7.1
                                                                                                                                                                                                   Mismatches
                                                 -YERARYRYNDNLVHESL--
                                                                                                                                                                                                              5; DB 1;
7.1e-05;
                                                                                                                                                                                                                                                                Glycosyltransferase
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                                                                                                                           ----TLYEPT----
                                                                                                                                                                                                                           Length
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Search completed: April Job time : 24 secs 17, 2003, 17:27:24

20.55	1 788 56.2 275 2 B70670 hypothetical 2 238.5 17.0 247 2 AG0376 probable glyc 3 232.5 16.6 260 2 E71975 hypothetical 4 231.5 16.7 259 2 F64532 conserved hyp	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.  SUMMARIES  Result Query No. Score Match Length DB ID	POST-processing: Minimum Match 0%  Maximum Match 100%  Listing first 45 summaries  Database: PIR_73:*  1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*	eq length: 0 eq length: 20000000	ext 0.5	Run on: April 17, 2003, 17:25:05; Search time 47 Seconds (without alignments) (without alignments) 544.080 Million cell updates/sec Title: US-09-705-911-24 Perfect score: 1401 Sequence: 1 MTAPVFSIIIPTFNAAVTLQALRTRLIRVKAVSKERSAEP 266	Copyright (c) 1993 - 2003 Compugen Ltd.  OM protein - protein search, using sw model
cal prote glycosylt ransferas ransferas cal prote glycosyl transfera cal prote	ים מי	rinted,				tes/sec	•

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	11.7	11.8	11.8	11.8	12.0	12.0	12.0	12.0	12.0	12.1	12.1	12.2	12.2	12.3	12.3	12.4
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	G71153	H64130	A84114	T44330	AE1876	AH1566	AH2189	A64099	G71148	AC1566	н96021	F95205	A70037	E89789	Q3ECTH	F86037
;	hypothetical prote	glycosyl transfera	glycosyltransferas	glycosyl transfera	hypothetical prote	galactosamine-cont		glycosyl transfera	probable glycosyl	hypothetical prote	probable glycosylt	glycosyl transfera	capsular polysacch	hypothetical prote	hypothetical 40.5K	probable regulator

#### ALIGNMENTS

Cross-references: GB:ZB3018; GB:AL123456; NID:g3261671; PIDN:CAB05419.1; PID:g1694 Experimental source: strain H37Rv Smith, D.R.; Robison, K. Smith, D.R.; Robison, K. Smith, D.R.; Robison, K. Description: Mycobacterium tuberculosis cosmid tbc2. Reference number: S73053 Accession: S73064 Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holr jandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. ture 393, 537-544, 1998
Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. Title: Deciphering the biology of Mycobacterium tuberculosis from the complete Reference number: A70500; MUID:98295987; PMID:9634230
Accession: B70670
Status: prellminary; nucleic acid sequence not shown; translation not shown Molecule type: DNA
Molecule type: DNA
Residues: 1-275 COLE Status: preliminary Molecule type: DNA Residues: 1-275 <SMI> lternate names: u0002kc protein
species: Mycobacterium tuberculosis
sate: 17-Jul-1998 #text\_change 20-Jun-2000
ccession: B70670; S73064 latches 156; uery Match uperfamily: Neisseria meningitidis glycosyl transferase A ene: Rv2957 ross-references: EMBL:U00024; NID:g560506; PIDN:AAA50938.1; PID:g560517 othetical protein Rv2957 - Mycobacterium tuberculosis (strain H37RV) 61 RLYVHSGPDDGPYDAMNRGYGVATGEWYLFLGADDTLYEPTTLAQVAAFUGDHAASHLVY 120 Local Similarity Conservative 56.2%; Score 788; DB 2; Length 275; 60.9%; Pred. No. 2.6e-64; 24; Mismatches 54; Indels 22; Gaps Holroyd 2 gen

80 RLIIHRDTDQGVYDAMNRGVDLATGTWLLFLGADDSLYEADTLARVAAFIGEHEPSDLVY 139

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Species: Helicobacter pylori
; Variety: strain J99
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C; Accession: E71975
R; Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; V
Nature 397, 176-180, 1999
A; Title: Genomic sequence comparison of two unrelated isolates of the human
A; Reference number: A71800; MUID:99120557; PMID:9923682
A; Accession: E71975
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A; Residues: 1-260 <ARN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Yersinia
C; Date: 02-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable glycosyltransferase wbyL [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
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                                                                                                                                                                                                                                                                     A; Status: preliminary
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A; Accession: AG0376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.;
Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: AG0376
                                                                                                                                                                                  ;Cross-references: GB:AE001448; GB:AE001439; NID:g4154594; PIDN:AAD05675.1; PID:g41546(
;Experimental source: strain J99
                                                                                                                                                                Genetics:
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                                                Matches
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                                                                    Local
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Local Similarity 32.2%;
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                                                                                                                                     jhp0094
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    SIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLVVHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ES--DQGIYDALNKGIDLATGDIIGFLHSDDLLAYPGALSDIVETF-EKQQCDAVYGDLQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIITATYNSERTISDTLSSLEKQTYLDVEYIIVDGASKDNTLTVISQNSTRV---TKIIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --STRLGIRLVIVLVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65;
                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pestis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
                                                                  16.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GFFNHEKMKYGWMPPHPTFYMKRDLYIRFGGFDLSYKISAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41;
                                           53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 238.5;
Pred. No. 3.
                                                                  Score 232.5;
Pred. No. 1.
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                                                Mismatches
                                                                  DB 2;
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                                                                                                                                                                                                                                                                                                                                                                            Taylor, D.E.; Vovis, G.F.;
                                           39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
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                                                                                                                                                                                                                                                                                                                                   the human gastric pat
                                           Gaps
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                                             <u>6</u>.
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                                                                                                                                                                                                  RESULT 5
AB2190
Nakazaki, N.; Shimpo, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic
                                                         C; Accession: AB2190
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.;
                                                                                                       A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
                                                                                                                                                  C; Species: Nostoc sp.
                                                                                                                                                                           hypothetical protein alr3073 [imported] - Nostoc sp. (strain PCC 7120)
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C;Accession: F64532
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, FR;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, FP Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; MCKeson, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.; Fujii, C.; Bowman, C.; Watthey, Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
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A; Residues: 1-259 < TOM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Start codon: TTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Date: 09-Aug-1997 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conserved hypothetical protein HP0102 - Helicobacter pylori (strain 26695)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: F64532
                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                             180
181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 RLFVVQKISFSYLKEVL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                        121 KPDCLEKVVRYYEIGEFNPKTLLYGVVPAHPTLFVKKAIYERYGLYKTDYKISADFEMII 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215
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                                                                                                                                                                             62 EKDEGIYDAMNKGIKRSSGDIIALLNSDD-FYKDEFVVEKVVHEFERKNCDSVYADLVFV
                                                                                                                                                                                                                        67 GPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYGDVVM- 125
                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                   7 SIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLVVHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYGDV--- 123
RLFVVQKISFSYLKEVL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRNKENLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPDCLEKVVRYYESGEFSPKTLLYGVVPAHPTLFVKKAIYERYGLYKTDYKISADFEMII 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----VMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRELFDGIGPYNLRYRVWADWDFNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVITACFNSEKTIEDTILSVLNQTYKNIEYIIIDGASADSTLEIIQKYKDRIA---CVMS
                                        RCFSNPALITRYMDVVI 196
                                                                                                                                                                                                                                                                      SVITACENSEKTIEDTILSVLHQTYKNIEYIIIDGASTDSTLEIIQKHRDKIA---CVMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RCFSNPALITRYMDVVISEYNDMTGFSMRQG--TDKEFRKRLPMYFWVAGWETCRRMLAF
                                                                                                                                   -----RSTKSRHAGPFDLDRLLFETNLCHQSIFYRRELFDGIGPYNLRYRVWADWDFNI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                   54;
                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GB:AE000532; GB:AE000511; NID:g2313184;
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                                                                                                                                                                                                                                                                                                                                                                46;
                                                                                                                                                                                                                                                                                                                                                                                      Score 231.5; DB 2;
Pred. No. 1.5e-13;
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                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                120
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S.; Sugimoto,

**X** .. the

Takazawa, Filamentous

Sasamoto, S.; Watanabe,

7120

Yasuda,

Nitrogen-fixing Yamada,

Cyanobacterium

Sequence of

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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
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A; Gene: alr3073
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                                                     DЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-321 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: AG2188
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A;Experimental source: strain PCC 7120
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A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 36...
66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Nostoc sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 MLAFLKDKENRRLALRTRLIRVKAVS 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 DWDFNIRCFSNPALITRYMDVVISEYNDMTGFSMRQGTDKEFRKRLPMYFWVAGWETCRR 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118
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                                                                    118 AYIDEQGKSTGKIFKNQVEGYVWPQLTEHNIVECGSVALVRRVCFEKMGLFDRNLGSYV- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 VHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLYYGDV 123
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                                                                                                                                                                                                                                                  64 VHSGPDDGPYDAMNRGVGVATGEWYLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYGDV 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                4 PVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLV 63
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                                                                                                                                                                                                                                                                                                                                                                PKVSVVIPAYNAMPYLPETLESVLRQTYHDFEVVVVNDGSSDNTEEWVSQI---LDPRLK 58
                                                                                                                                        VMRSTKSRHAGPFDLDRL------LFETNL--CHQSIFYRRELFDGIGPY--NLRYRVW 172
                                                                                                                                                                                                                    LISQANQGLAGARNTGIVNASGEYIAFLDADD-IWEPTKLAKQVSVLDENPTVGLVYTWV
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ADWDENIRCESNPALITRYMDVVISE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.8%; Score 207; DB 2; Length 321; 32.0%; Pred. No. 3.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35; Mismatches
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Pred. No. 2.3e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 324
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DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A:Reference number: AB1807; MUID:21595285; PMID:11759840
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R;KaneKo, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glycosyl transferase PAB0772 - Pyrococcus abyssi (s
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999
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A;Residues: 1-316 <KUR>
A;Residues: 1-316 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB74767.1; PID:g17132162; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A; Accession: AE2189
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                                                                                                                                                                                                     C; Superfamily: Neisseria meningitidis glycosyl transferase
                                                                                                                                                                                                                                                                                 A; Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-298 <KAW>
                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A; Accession: B75096
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Description: Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, July 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; anonymous,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          в75096
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                                                                                                                                                Query Match
                                                                                                                                                                                                                                                          Genetics:
                                                                                                                                                                                                                                                                                                    Cross-references: GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB50071.1; PID:g54
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                                               1 MTAPVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGS 60
                                                                                                                                                                                                                                  PAB0772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          abyssi genome sequence: insights into
                                                                                                                           14.7%; Score 205.5; DB 2 29.0%; Pred. No. 4.3e-11;
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                                                                                                 Mismatches
                                                                                                                                                   DB 2;
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                                                                                                                                                   Length
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                                                                                                                                                      298;
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Rajandream, M.A.; Rogers, J.; Kuller, J., Rajandream, M.A.; Rogers, J.; Kuller, J., Rajandream, M.A.; Rogers, J.; Kuller, J., Rajandream, M.A.; Barrell, B.G. Nature 393, 537-544, 1998

Nature 393, 537-544, 1998
                                                                                                                                                                                               hypothetical protein Rv1514c - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Ju1-1998 #sequence_revision 17-Ju1-1998 #text_change 22-Oct-1999 C;Accession: E70714 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; HG Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazav
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A; Title: Complete Genomic
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; Pred. No. 6e-11;
48; Mismatches 8
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A; Experimental source: strain F
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A; Residues: 1-262 <COL>
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A; Status: prelimina
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                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-337 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakazaki, N.;
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Best Local Similarity
183
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AAQDRDFFLSVVMNGAKVAYQPGCYAYYRRYGSVTVS
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                                                                                                                          YPQQGGNHARNRGFELSQGEYIQYLDADDYIL-PEKIEKQVNFL-ETTGADVVYGD----
                                                                                                                                                      GPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYGDVVMR 126
                                                                                                                                                                                       SVIIPCFNAEKWIREAIESCLTQTYADVEIIVIDDGSTDNSLEIIKTF----GNEIIWRS
                                                                                                                                                                                                                     SIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLVVHS
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                                                           WRHQRHL-PDDSSFLDKIEISGVQADILAALLANWWVALAALMYKRSVVENSDRWDETLP
                                                                                           STKSRHAGPFD---LDR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                              enomic Sequence of the Filamentous Nitrogen-fixing AB1807; MUID:21595285; PMID:11759840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y.; Wolk, C.P.; Kuritz, T.;
.; Sugimoto, M.; Takazawa, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.5%;
                                                                                                                                                                                                                                                                  14.0%; Score 196.5; DB 28.1%; Pred. No. 3.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [imported] -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; GB:AL123456;
H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acid sequence not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 202.5; DB 2; Pred. No. 6.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                      Mismatches
                                                                                         ---LLFETNLCHQSIFYRRELFDGIGPYNLRYR 170
                               -RYMDVVIS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nostoc sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NID:g3261635;
219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             shown;
                                                                                                                                                                                                                                                                                                                                                                PID:g17130260;
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08
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M.; Yamada, M.;
                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                                                                                                                   337;
                                                                                                                                                                                                                                                   37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         strain PCC
30-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                    GSPDB:GN00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Watanabe,
; Yasuda, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyanobacterium
                                                           182
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                                                                                                                          123
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                                                                                                                                                                                                                                                   8;
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RESULT -\97168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lycosyltransferase [imported] - Clostridium acetobutylicum
;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: A97168
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Experimental source: strain 1021, megaplasmid pSymB R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hübler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T. Cience 293, 668-672, 2001

;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weldner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                            : Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4818, 2001
A; Title: Genome Sequence and Comparative Analysis of the A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Accession: A97168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
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A;Title: The complete sequence of the 1,683-kb psymB megaplasmid A;Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-336 <KUR>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-367 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A95842; A; Accession: G95948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: G95948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AL591985; PIDN:CAC49255.1; PID:g15140741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                       A; Experimental source: Clostridium
                                                                                                                                                                                                                                               Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RLVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAAS---- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \vdash
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     σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIDMLIGNRIIRGKPNPIYRPGSLRILSMFFTIFMHSTVVYNRNV---IPEEMLRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --HLVYGDVVMRSTKSRHAGPFDLDRL-LFETNLCHQSIFYRRELFDGIGPYNLRY 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MPTPVVSIVLPVYNAEPYIAAAIESVLRQDYERLEVIAIDDGSTDRSRDILERYR-KSDS
                           PVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVSIISRENRGLIATLNEGLALAKGELIARMDADDIAYPSRLSRQVALFSAEPRLALSGT
PKVSIVMPVYNSERYLAEAIESILDQTYNDFEFIIVDDGSTDESYNIISSYANK-DNRII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
                                                                                                          Similarity
65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                          Conservative
                                                                                                                                                                                                                                                                  GB:AE001437; PIDN:AAK80132.1; ce: Clostridium acetobutylicum
                                                                                                                                  13.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.0%; Score 196.5; DB 2; 30.7%; Pred. No. 3.7e-10; Live 33; Mismatches 78;
                                                                                                          57;
                                                                                                       Score 192; DB 2; 1
Pred. No. 8.5e-10;
57; Mismatches 113;
                                                                                                                                                                                                                                                                  PID:g15025168;
ATCC824
                                                                                                                                                        Length
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                                                                                                          40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q.; Gibson,
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RESULT 15 AD2189

hypothetical protein alr3067 [imported] - Nostoc sp. (strain PCC C;Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. sC;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 3

C; Accession: AD2189
R; Kaneko, T.; Nakamura,
Nakazaki, N.; Shimpo, S
DNA Res. 8, 205-213, 200

, Y.; Wolk, C.P.; Kuritz, T.; S.; Sugimoto, M.; Takazawa, N

**X** :.

Sasamoto,

X . . .

Watanabe, ; Yasuda,

A .

; Irig Tabat

**X** ::

Cyanobacterium

strain 30-Jun-

PCC -

A;Accession: AD2189 A;Status: prelimina

A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing A; Reference number: AB1807; MUID:21595285; PMID:11759840

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DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2160
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                                                                                                                                                                              B
                                                                                                                                                                                                                                                                                                                                    A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB:BA000019; PIDN:BAB74535.1; PID:g17131930; GSPDB:GN00179 A; Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-322 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Note: Nostoc sp. strain PCC 7120 is a C; Date: 14-Dec-2001 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glycosyltransferase alr2836 [imported] - Nostoc sp. (strain C.Species: Nostoc sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: AE2160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakazaki, N.;
                                                                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                         Genetics:
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183
                            173 AD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 A---FGDIDEKQKTIYNSAFSIKFDSQNIEQVFLTSCAIPHPSVMFKKDSIVKLRGYRKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
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                                                                                                                    64 QANQGQGGAFNAGFAAATGEVVAFLDADD-VWKPHKLQRIVEVFQTSDVVGVMHHLDIID 122
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                                                          GNDKTIDQASTQGPKLSEDLASVILQTGNAWCFPPTSGLAYRREVLEKVFPIDPVKWRIW
                                                                                       RSTK----SRHAGP----FDLDRLLFETN--LCH---QSIFYRRELFDGIGPYN-LRYRVW
                                                                                                                                     SITIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLVVHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NDTNKKDKVDYLIWGASTGGKLVKKVVESTTDKFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YDTAEDYDLWLRAIRNGYKIVR-MDECLIKYRVHNKSKTAVEMFNPKMVEYTMKAKIDYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YRVWADWDENIRCESNPALITRYMDVVISEYN------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VISREHRGLVDSLNEGINIARGKYIARMDADDISINNRIEKQFEFLELNKDVDILGTRIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YHSGPDDGPYDAMNRGYGYATGEWYLFLGADD-----
                                                                                                                                                                              SVIISNYNYARYLSRAINSVLAQTHSDIEIVIVDDGSTDNSRDVITQLQEQAPDKIKPIF
                            174
                                                                                                                                                                                                                                                           Similarity
184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shimpo,
                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       strain PCC 7120 is a synonym of 1 #sequence_revision 14-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S.; Sugimoto, M.;
                                                                                                                                                                                                                                                         13.6%; Score 190.5;
29.1%; Pred. No. 1.
                                                                                                                                                                                                                                            39;
                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kuritz, T.; Sas
; Takazawa, M.;
                                                                                                                                                                                                                                                         .1e-09;
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M.; Yamada, M.; Yasuda,
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Search completed: April 17, 2003, 17:28:55 Job time : 56 secs
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A;Residues: 1-323 <KUR>
A;Residues: 6B:BA000019; PIDN:BAB74766.1; PID:g17132161; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: alr3067
                                                                                                                                                                                                                                                                                                                                    Query Match 13.6%; Score 190.5; DB 2; Best Local Similarity 22.2%; Pred. No. 1.1e-09; Matches 53; Conservative 44; Mismatches 69;
                                                          165 LIRRAAIDSVGLFDPTLKSCEDWDFYLRLAAWQFALVKKAQIIYRQSPTAMTSKLDVM 223
                                                                                               128 YKFANEADSYADESNSFAGD------VYAELLIKNFLQNGSNP------ 164
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# ALIGNMENTS

# RESULT 1 AAW21774

AAW21774 standard; Protein; 266 AA.

AAW21774;

11-MAR-1998 (first entry)

Protein encoded by ORF F of GS region in M. avium subspecies silvaticum.

GS; pathogenecity island; pathogenic protein; mycobacterial disease; cellular recognition receptor; pathogenic mycobacteria; Crohn's disease; vaccine; inflammatory disease; sarcoidosis; Johne's disease.

Mycobacterium avium subspecies silvaticum

XSX WO9723624-A2

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XYXX 03-JUL-1997.

23-DEC-1996;

Result

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Score 1401 1401

Match

Length

DB IJ

Description

Query

205.5 202.5 201.5

AAW88309 AAB96313 AAW21779 ABP26805 AAW88314 AAY54072 AAY43774

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AAW21775 AAW21783 AAW21774

Protein encoded by Protein encoded by Protein encoded by E coli colitose o Putative glycosylt Protein encoded by

Streptococcus poly Sugar transferase Enzyme EPS8 which

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acid

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186 186

21-DEC-1995; 95GB-0026178. 96WO-GB03221

(SGEO-) ST GEORGE'S HOSPITAL MEDICAL SCHOOL.

Doran T, Ford J, Sumar N, Tizard M; Hermon-Taylor J, Loughlin M, Millar D;

WPI; 1997-351061/32. N-PSDB; AAT74469.

New isolated pathogenicity island from mycobacteria used ç

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RESULT 2
AAW21775
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                     GS; pathogenecity island; pathogenic protein; mycobacterial disease; cellular recognition receptor; pathogenic mycobacteria; Crohn's disease. vaccine; inflammatory disease; sarcoidosis; Johne's disease.
                                                                                             03-JUL-1997
                                                                                                                                                           Mycobacterium
                                                                                                                                                                                                                                                                                                                                                  AAW21775 standard; Protein; 266
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                                                                                                                                                                                                                                                     Protein encoded by ORF F of the GS region in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            develop products for detection, diagnosis, prevention and treatment
                               21-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                           paratuberculosis
                              95GB-0026178.
                                                             96WO-GB03221
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Pred. No. 7.3e-144;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                266
                                                                                                                                                                                                                                                   M. paratuberculosis
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The present sequence represents a protein encoded by open reading frame (ORF) F of a novel polynucleotide sequence designated "GS". GS is a pathogenecity island of 8 kb of DNA comprising a core region of 5.75 kb with multiple ORFs and an adjacent transmissable element of 2.5 kb. The CORFs, and also the transmissable element, encode proteins which may be linked to pathogenecity. Such as providing receptors for cellular recognition. GS was discovered and characterised using differential DNA analysis technology. It is found within Mycobacterium paratuberculosis and it has also been identified in Mycobacterium avium subspecies and the intestine and Crohn's disease in humans. The protein products of the intestine and Crohn's disease in humans. The protein products of the intestine and Crohn's disease in particular they can be used for detecting mycobacteria or for diagnosing, treating or preventing mycobacterial disease. In particular they can be used as vaccines for inflammatory diseases such as Crohn's disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Doran
Sumar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-351061/32.
N-PSDB; AAT74470.
                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 51; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                         of mycobacteria infections
                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated pathogenicity island from mycobacteria - develop products for detection, diagnosis, prevention
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Tizard 1
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. В δÃ Query Match Best Local Sin Matches 266; Sequence \_ I MTAPVESIIIPTENAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSERPELGS MTAPVFSIIIPTENAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSERPELGS Similarity 266 AA; Conservative 100.0%; 0; Score 1401; DB 18; Pred. No. 7.3e-144; ); Mismatches 0; 0; Gaps 60 60 0

sarcoidosis

in humans or Johne's disease in animals.

밁 δÃ 밁 Ş 121 121 61 61 GDVVMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRELFDGIGPYNLRYRVWADWDFNIR 180 RLVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVY 120 GDVVMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRELFDGIGPYNLRYRVWADWDFNIR RLVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVY 120

181 181 

240 240

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RESULT

241 241 KENRRLALRTRLIRVKAVSKERSAEP KENRRLALRTRLIRVKAVSKERSAEP

> 266 266

AAW21783 AAW21783; AAW21783 standard;

Protein;

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11-MAR-1998

Protein encoded by ORF F from (first entry) the GS region of M. tuberculosis

GS; pathogenecity island; pathogenic protein; mycobacterial disease; cellular recognition receptor; pathogenic mycobacteria; Crohn's disease; vaccine; inflammatory disease; sarcoidosis; Johne's disease; ss.

(SGEO-)

ST GEORGE'S

HOSPITAL MEDICAL SCHOOL

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RESULT 4
AAW88309
ID AAW8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                analysis technology. It is found within Mycobacterium paratuberculosis and it has also been identified in Mycobacterium avium subspecies silvaticum. These pathogenic mycobacteria cause chronic inflammation of the intestine and Crohn's disease in humans. The protein products of the ORFs of GS can be used for detecting mycobacteria or for diagnosing, treating or preventing mycobacterial disease. In particular they can be used so received as a crohn's disease or because of the contract of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents the protein encoded by open reading frame (ORF) F, from M. tuberculosis. This ORF F has been found to have homoogy with ORF F of a novel polynucleotide sequence designated "GS" GS is a pathogenecity island of 8 kb of DNA comprising a core region of 5.75 kb with multiple ORFs and an adjacent transmissable element of 2.5 kb. The ORFs, and also the transmissable element of element of 2.5 kb. The linked to pathogenecity, such as providing receptors for cellular recognition. GS was discovered and characterised using differential DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated pathogenicity island from mycobacteria - used to develop products for detection, diagnosis, prevention and tre of mycobacteria infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Doran T,
Sumar N,
                                                                                                                                   AAW88309 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 56; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-1996;
                           26-APR-1999
                                                                                 AAW88309;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MTAPVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDVVMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRELFDGIGPYNLRYRVWADWDFNIR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVY 120
                                                                                                                                                                                                                                                                                                                                                                                                                              CFSNPALITRYMDVVISEYNDMTGFSMRQGTDKEFRKRLPMYFWVAGWETCRRMLAFLKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDVIMRSTNFRWGGAFDLDRLLFKRNICHQAIFYRRGLFGTIGPYNLRYRVLADWDFNIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAAPMFSIIIPTLNVAAVLPACLDSIARQTCGDFELVLVDGGSTDETLDIANIFAPNLGE 79
                                                                                                                                                                                                                                                                                                                                                                              CFSNPALVTRYMHVVVASYNEFGGLS-NTIVDKEFLKRLPM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLIIHRDTDQGVYDAMNRGVDLATGTWLLFLGADDSLYEADTLARVAAFIGEHEPSDLVY
                                                                                                                                                                                                                                                                       --STRLGIRLVIVLVR 253
                                                                                                                                                                                                                                                                                                                            KENRRLALRTRLIRVK 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 AA;
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                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            humans or Johne's disease in animals.
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                                                                                                                                   Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.2%;
60.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                   297
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Pred. No. 4e-77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Loughlin
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                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                               This is the amino acid sequence of the protein encoded by the wbdL gene of a gene cluster (see AAX06748) involved in the biosynthesis of the Escherichia coli Olli O antigen. The protein shows low homology with Lsi2 of Netsseria gonorrhoeae, and is predicted to be a colitose or glucose transferase. The use of nucleic acid molecules derived from particular assembly and transport genes, particularly wbd (transferase), wzx (flippase) and wzy (polymerase) genes, within O antigen gene clusters improves the specificity of methods for the detection and identification of O antigens, e.g. in testing food- or faecal-derived samples, or samples from patients. The O antigen is a major virulence factor of enteropathogenic E. coli strains that cause diarrhoea and haemorrhagic colitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O antigen; Olll antigen; wbdL gene; colitose transferase; glucose transferase; diarrhoea; haemorrhagic colitis; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid molecules specific for bacterial polysaccharide antigens - useful for detecting specific strains in, e.g. for faeces or patient samples
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N-PSDB; AAX06748.
                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 7; 165pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1997;
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239
                                                          185
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                                                                                                                       132
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                         212 DKEFRKRLPMYFWVAGWETCRRMLAFLKDKENRRLALRTRLI 253
                                                                                                                                                                                   72
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                                                                                                                                                                                                                                             15 LDAPLVSIIIATYNSELDIAKCLQSVTNQSYKNIEIIIMDGGSSDKTLDIAKSFKDD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coli colitose or glucose transferase
                                                                                                                                                                                                                                                               TLE-
                                                                                                                                                   GDVVMRSTKSRHAGP------FYRREL
                                                                                                                                                                                                                RLVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVY 120
                                                                                     FDGIGPYNLRYRVWADWDFNIRCF----SNPALITRYMDVVISEYNDM-TGFSMRQGT
                                                                                                                      G-----RTAHEGPDRNISGFSGSEWYNLTGFKFNYYKCNLPLPIMSAIYSRDFFRNER
                                                                                                                                                                                  RIKIVSEKDRGIYDAWNKAVDLSIGDWVAFIGSDDVYYHTDAIASLMXGVMVSNGAPVVY
                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                        297 AA;
                                                          --IKLKIVADADWFLRCFIKWSKEKSPYFINDTTPIVRMGYGGVSTDISSQVKT
                                                                                                                                                                                                                                                                                                             Conservative
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97AU-0006545
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                                                                                                                                                                                                                                                                                                                        21.38; 27.78;
                                                                                                                                                                                                                                                                                                           52;
                                                                                                                                                                                                                                                                                                           Score 298; DB 20;
Pred. No. 9.4e-24;
2; Mismatches 86;
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                                                                                                                                                                                                                                                                                                                                      Length 297;
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                           66;
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                       211
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8

RESULT 5
AAB96313
ID AAB9
XX

AAB96313 standard; Protein; 298

AAB96313;

AAW21779;

11-MAR-1998

(first entry)

Protein encoded by

ORF B from

the GS

region of M.

tuberculosis

GS; pathogenecity island; pathogenic protein; mycobacterial disease; cellular recognition receptor; pathogenic mycobacteria; Crohn's disease; vaccine; inflammatory disease; sarcoidosis; Johne's disease; ss.

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                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 71
                                                                                                                                                                                                                                                                                                                                                The present invention relates to the genomic sequence of pyrococcus abyssi (see AAF86431 and AAH41233-7) and P. abyssi proteins. P. abyssi a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up 110 degrees centigrade.

Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436.
                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; Pages 981-982; 1657pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleotide sequences isolated proteins useful in industry -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Forterre P,
Querellou J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyrococcus abyssi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hyperthermophilic archaeon; hyperthermophilic protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-OCT-2001
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227
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                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                              MTAPVESIIIPTENAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGS 60
                                                                                                      GVVYGGFYYVSQDGRILGKRLPKHRGDI-YSHLLKENFIGSPTLLIRRECFKKAGLFDPR
                                                                                                                                 HLVYGDVVMRSTKSR------HAGPFDLDRLLFETNLCHQSIFYRRELFDGIGPYNLR 168
                                                                                                                                                                                     ----RLVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAAS 116
                                                                                                                                                                                                               HLDIW 231
                         RLPMY 222
                                                 LSSSQDWDMWLR-----
                                                                            YRVWADWDFNIRCFSNPALITR----YMDVVISEY---NDMTGFSMRQ---GTDKEFRK 217
                                                                                                                                                          IRYIRLKKNSG----GPI-ARNIGIKKAKGRFIALLDDDDEWLPHRLEVQVRKFENLGKEF 114
                                                                                                                                                                                                                                                                                                                          298 AA;
                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thierry JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weissenbach J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99FR-0005034.
                                                                                                                                                                                                                                                                               14.7%; Score 205.5; DB 2
29.0%; Pred. No. 1.1e-13;
                                                 IARYYKFDYVDEIIAKYYVHGKQISFNMKKYIPGRERLIRK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prieur D,
                                                                                                                                                                                                                                                                      38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eur D, Dietrich J,
Saurin W, Heilig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            involved in cell wall biogenesis #1.
                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from Pyrococcus
                                                                                                                                                                                                                                                                                             DB 22;
                                                                                                                                                                                                                                                                      99;
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                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encode
                                                                                                                                                                                                                                                                    37;
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                                                                                                                                                                                                                                                                    Gaps:
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RESULT 6
AAW21779
ID AAW2

AAW21779 standard; Protein; 262

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В δÃ

119

120 62 61

QY

DFNIRCFSNPALITRYMDV--VISEYNDMTG

WGFGMDRLVGLDRVRGPIPFSLRKFLAGKQVVPHQASFFGSSLVAKIGGYDLDFGIAADQ

179 176

EFILRA---

-ALVCEPVTIRCVLCEF-DTTG

204 204 Ş 밁 Š

SAPTVSVITISFNDLDGLQRTVKSVRAQRYRGRIEHIVIDGGSGDDVVAYLSGCEPGFA-

61 60

RLVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQ-VAAFLGDHAASHLV 119

--YWQSEPDGGRYDAMNQGIAHASGDLLWFLHSADRFSGPDVVAQAVEALSGKGPVSEL-YG---DVVMRSTKSRHAGPFDLDRLLFETNLC-HQSIFYRRELFDGIGPYNLRYRVWADW 175

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Matches Query Match Best Local

68;

Conservative

14.5%;

; Score 202.5; ; Pred. No. 1.9e 36; Mismatches

.9e-13 DB 18; 90;

Indels

17; Gaps

9;

Length 262;

Local Similarity

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The present sequence represents the protein encoded by open reading frame CC (ORF) B, from M. tuberculosis. This ORF B has been found to have homogy CC with ORF B of a novel polynucleotide sequence designated "CS". GS is a cc pathogenecity island of 8 kb of DNA comprising a core region of 5.75 kb with multiple ORFs and an adjacent transmissable element of 2.5 kb. The CC With multiple ORFs and an adjacent transmissable element, encode proteins which may be clinked to pathogenecity, such as providing receptors for cellular cc recognition. GS was discovered and characterised using differential DNA CC analysis technology. It is found within Mycobacterium paratuberculosis cr and it has also been identified in Mycobacterium avium subspecies cs conditation. These pathogenic mycobacteria cause chronic inflammation of the intestine and Crohm's disease in humans. The protein products of the ORPs of GS can be used for detecting mycobacteria or for diagnosing, creating or preventing mycobacterial disease. In particular they can be used as vaccines for inflammatory diseases such as Crohm's disease or cycles as croidosis in humans or Johne's disease in animals.
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Sumar N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated pathogenicity island from mycobacteria -develop products for detection, diagnosis, prevention of mycobacteria infections
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
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N-PSDB; AAT74473.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 53; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ford J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tizard M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΧX
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                                                                                                                                                                                                                                                                                                                                                                                                                                        CC The invention relates to a protein (ABP25413-ABP30895) from group B CC streptococcus/BBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in CC the specification. The proteins have antibacterial and antinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by CC Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. CC Nucleic acids encoding (I) are used to detect Streptococcus in a CC biological sample. (I) is used to detect Streptococcus in a CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP26805
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                                                                                                                                                                                                                                                                                 Best
                                                                                                                                                                                                                                                                                                          Query Match
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24-NOV-2000;
07-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 3429; 4525pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-352536/38
N-PSDB; ABN67436.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAY-2002
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                                                                                                                                                   SIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLVVHS 66
KNNGGLSDARNYGISRATGDYIYLLDSDDYLYKEDAIERMVEF-SEKYNSEIVLGCYVEK
                                                     GPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYG-----
                                                                                                                       SIIIPVYNVQSFLNECIESVLAQTYSNLEIILVNDGSTDNSGDICD-YYSEIDGRIFVFH
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INST GENOMIC RES.
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                                                                                                                                                                                                                                                                                                                                                                      321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000GB-0026333.
2000GB-0028727.
2001GB-0005640.
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                                                                                                                                                                                                                                               33;
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                                                                                                                                                                                                                                           Score 201.5; DB Pred. No. 3.4e-13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the amino acid sequence of a sugar transferase that is encoded by the wbd0 open reading frame of a gene cluster (see AAX06749) involved in the blosynthesis of the Escherichia coil 0157 0 antigen. The use of nucleic acid molecules derived from particular assembly and transport genes, particularly wbd (transferase), wzx (flippase) and wzy (polymerase) genes, within 0 antigen gene clusters improves the specificity of methods for the detection and identification of 0 antigens, e.g. in testing foodor faecal-derived samples, or samples from patients. The 0 antigen or faecal-derived samples from patients. The 0 antigen or samples from patients. The 0 antigen or samples from patients.
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diarrhoea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigens - useful for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid molecules specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-059669/05
N-PSDB; AAX06749.
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01-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-APR-1999
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                                                      126 RSTKSRHAGPFDLDRLL-----FETNLCHQSIFYRRELFDGIGPYNLRYRVWADWDFN 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 REQHIINIVLEDEMIETISPVQAIQNIYNYDAYRAIF--TVAHNKL-YKRELF
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                                                                                                                                                                                                                                                                                           7 SIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLVVH- -65
KEPCLIKVGLFENDKLLGFSSITHSNTGYCHQGVIFPKNHSE----YDLRYKICADYKLI 155
                                                                                                                      YEKDEGIYDAMNKGRMLAKGDLIHYLNAGDSV--
                                                                                                                                                                       SGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYGDVVM 12:
                                                                                                                                                                                                                                    SVITVTYNNAEGLEKTLSSLSILKIKPFEIIIVDGGSTDGTNRVISRFT----SMNITHV 59
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                                                                                                                                                                                                                                                                                                                                                        l Similarity
67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or patient samples
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---DVVMRSTKSRHAGP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang
                                                                                                                                                                                                                                                                                                                                                        Conservative
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97AU-0006545.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and haemorrhagic colitis
                                                                                                                                                                                                                                                                                                                                                        42;
                                                                                                                                                                                                                                                                                                                                                     Score 190; DB 20;
Pred. No. 4.1e-12;
2; Mismatches 80;
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Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                     AAY54065-74 represent enzymes involved in the biosynthesis of exopolysaccharides (EPS). These enzymes are designated EPS1-EPS10. and are encoded by open reading frames eps1-eps10. The enzymes are isolated from Streptococcus thermophilus strain Sfi39. The proteins are used in a method for the synthesis of EPS, which includes at least one step of forming a bond (alpha or beta-isomer) between C-1 (carrying the reducing aldehyde function, of an activated D-galactose pyranose), and the content of the synthesis of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-APR-1998;
22-APR-1998;
.22-APR-1998;
                                            a phosphate on a lipophilic or proteinaceous primer. Stepwise synthesis of EPS occurs with, in each step, addition of a new sugar unit, through its hemi-acetyl function, to an alcoholic hydroxyl of a second sugar unit, present at the end of a chain of sugar residues bonded to the primer. EPS1 to EPS4 are used to elongate the EPS chain, and to regulate EPS production, EPS5 creates new bonds between saccharides, EPS6 is used in the blosynthesis of EPS, EPS7 and EPS8 are beta-glycoxyltransferases, EPS9 is a transporter of repetitive units, and EPS10 catalyses the conversion of a pyranose form of a beta-D-galactose to the furanose form. The EPS enzyme are used to improve properties of foods, particularly fermented milk products such as yoghurt and cheese, e.g. their organoleptic properties and flavour stability.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 105-106; 162pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Exopolysaccharide; EPS; ESP enzyme; EPS1; EPS2; EPS3; EPS4; EPS5; EPS6; EPS7; EPS8; EPS9; EPS10; Streptococcus thermophilus strain Sfi3 activated D-galactose pyranose; saccharide; beta-glycosyltransferase; transporter; food; fermented milk product; yoghurt; cheese;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant enzymes for synthesis of exopolysaccharides, particularly in lactic acid bacteria, for improving propertifermented milk products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-097267/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 flavour stability; organoleptic property.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPS8
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98EP-0201311.
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Query Match

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RESULT 10
AAY43774
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Streptococcus thermophilus Sfi39. The operon contains 10 open reading frames, and encodes enzymes (eps1, eps2, eps3, eps4, eps5, eps6, eps7, eps8, eps9 and eps10) that are involved in the biosynthesis of exopolysaccharides (EPS). The enzymes catalyse the formation of specific intersugar bonds. The enzymes catalyse a process that includes at least one step of forming a bond (in alpha or beta anomeric form) between C1, carrying the reducing aldehyde group of an activated D-Galp (galactose in pyranose form), and a phosphate group on a lipophilic or proteinaceous primer. The enzymes are used to produce EPS that have antitumor or probiotic properties or are used in foodstuffs to improve organoleptic qualities and flavour. When expressed by lactic accidence.
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22-APR-1998;
22-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eps operon; Streptococcus thermophilus Sf139; enzyme; eps3; eps4; eps5; eps6; eps7; eps8; eps9; eps10; exopolysaccharide biosynthesis; EPS; intersugar bond; problotic; foodstuff; organoleptic quality: flavour.
                                                                                                                                                                                                                                                                                                                                           Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant enzymes for biosynthesis of exopolysaccharides having e.g. antitumor or probiotic properties or useful in fermented milk
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                                                                                                                                                                                                                                                                                                                                                                                           products
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of eps8 of Streptococcus thermophilus Sfi39.
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                                                                                                                                                                                                                                                                                                                                      Page 106-107; 163pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             foodstuff;
d bacteria;
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98EP-0201311.
98EP-0201312.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organoleptic quality; flavour; acidified milk product; yoghurt;
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ality; flavour;
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Matches
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The present sequence represents a protein encoded by open reading frame (ORF) B of a novel polynucleotide sequence designated "GS". GS is a pathogenecity island of 8 kb of DNA comprising a core region of 5.75 kb with multiple ORFs and an adjacent transmissable element of 2.5 kb. The ORFs, and also the transmissable element, encode proteins which may be linked to pathogenecity, such as providing receptors for cellular recognition. GS was discovered and characterised using differential DNA analysis technology. It is found within Mycobacterium paratuberculosis and it has also been identified in Mycobacterium avium subspecies
                                                                                                                                             New isolated pathogenicity island from mycobacteria - develop products for detection, diagnosis, prevention of mycobacteria infections
                                                                                                                                                                                                                                                                                                                                        03-JUL-1997
                                                                                                                                                                                                                                                                                                                                                              W09723624-A2
                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                        GS; pathogenecity island; pathogenic protein; mycobacterial cellular recognition receptor; pathogenic mycobacteria; Cro
                                                                                                                        Claim 1;
                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                 Sumar
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DB; AAT74462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RYR---VWADWDFNIRCFSNPALI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSFRDFNGNIPKGWVPDFNVPTNYGTIVLDQFL-SSNISFVVWSSIYR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDV------VMRSTKSRHAGPFDLDRLLFETNLCH--QSIFYRRELFDGIGPYNL
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59; Conserv
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                                                                                                                       Page 45;
                                                                                                                                                                                                                                                                                                                                                                                                           inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                               Ford J, I
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                                                                                                                                                                                                                                                               GEORGE'S HOSPITAL MEDICAL SCHOOL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 AA;
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                                                                                                                    62pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                          Hermon-Taylor J,
                                                                                                                                                                                                                                                                                                                                                                                     subspecies
                                                                                                                                                                                                                                                                                                                                                                                                           receptor;
y disease;
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                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          of GS
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Pred. No. 1.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                           pathogenic mi
sarcoidosis;
                                                                                                                                                                                                                                                                                                                                                                                     silvaticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                         region in M. avium
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                                                                                                                                                                                                                                          Loughlin
                                                                                                                                                                                                                                                                                                                                                                                                                     mycobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                        disease;
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the intestine and Crohn's disease in humans. The protein products of ORFs of GS can be used for detecting mycobacteria or for diagnosing, treating or preventing mycobacterial disease. In particular they can used as vaccines for inflammatory diseases such as Crohn's disease or sarcoidosis in humans or Johne's disease in animals.
                                                                                                                                                                      02-FEB-2000;
16-OCT-2000;
                                                                                                                                                                                                                                                                                                 EPS plasmid; Lactococcus lactis subspecies cremoris Ropy352; exopolysaccharide; EPS352; milk; thickener; glycosyltransferbiosynthesis; fruit juice.
                                                                             WPI; 2001-488889/53.
N-PSDB; AAH43198.
                                                                                                                                    (UYOR-)
                                                                                                                                                                                                         02-FEB-2001; 2001WO-US03404
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                                                                                                                                                                                                                                                                                                                                                                                                                    AAB47426 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                             Lactococcus lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGGRRVSW----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GYGKNNLVGLDGKPLFPRPYGYMPFKMRKFLLGATVAHQATFFGASLVAKLGGYDLDFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G----DVVMRSTK---SRHAG--PFDLDRLLFETNLCHQSIFYRRELFDGIGPYNLRYRV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --YWQSQPDNGRYDAMNQGIAHSSGDLLWFMHSTDRFSDPDAVASVVEALSGHGPVRDLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RLVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVY 120
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                                                                                                              JE,
                                                                                                                                    UNIV OREGON STATE.
US DEPT OF AGRICUI
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2000US-0241098.
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27.3%;
                                                                                                              EP,
                                                                                                              Sandine
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Pred. No. 1.3e-11;
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                                                                                                            Ahlgren
                                                                                                                                                                                                                                                                                                             glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258
                                                                                                              JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                              Dierksen
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the
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New bacterium useful in pharmaceutical formulations, beauty cosmetics, comprises characteristics of Lactocremoris Ropy 352 -

Lactococcus

food

products s lactis

and

Claim 28; Page 67-68;

73pp;

English

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmid derived from L. lactis subspecies cremoris Ropy352. The EPS plasmid is about 32 kb in size and encodes at least 13 active genes. The enzymes encoded by these genes allow the bacteria to produce an exopolysaccharide, designated EPS352. When EPS352 is expressed in or added to milk, it imparts highly desirable sensory characteristics to the milk, including making the milk very thick, with a very smooth mouth-feel, and slightly sweet with an obvious chewable-bite. Open reading frames (ORF's) M and N show homology to glycosyltransferase involved in EPS352 is biosynthesis. L. lactis cremoris Ropy352 is deposited with the USDA-ARS-NCAUR-NRRL as deposit accession number NRRL B-30229. EPS352 is useful for thickening a liquid selected from milk, a milk-based liquid, a whey-based liquid, a soy-based liquid, a fruit-juice. It is also useful as an additive in pharmaceutical
                                                                                                                                                                                                                                                                                 Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                  27-OCT-2000; 2000GB-0026333
24-NOV-2000; 2000GB-0028727
07-MAR-2001; 2001GB-0005640
                                                                                                                                                                                                                                                                                                                                                         Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequences plasmid derive
Telford J,
                                                                                                                                                                                                                       WO200234771-A2
                                                                                                                                                                                                                                                     Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP26804 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               · 164 PYNLRYRVWADWDFNIRCFSNPALIT----RYMDVVISEYNDMTGFS------MRQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                     29-OCT-2001; 2001WO-GB04789
                               (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 TDKEFRKRLP--MYFWVAGWETCRRMLAFLKDKENRRLALRTRLIRVKAVSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 YNTKNIGVSHARNYGIDRASGSYIMFLDPDDT-YDKSYCLEMIGLINKFNA-----DVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KFNESINYLEDMLFNISIVHNARIIAYTNKRHYFYLQREDSASKKFSKSFFKSLNLIRGK 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jences given in AAB47426-27 are encoded by a fragment derived from L. lactis subspecies cremeria are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       beauty care products and coating agents.
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Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                        polypeptide SEQ ID NO
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Pred. No. 2.
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δÃ
                                       Best Loc
Matches
                                                                           Query Match
                                                                                                                                                                  Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds t (I). A composition comprising (I) or a nucleic acid encoding (I), may used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated me meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                          streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 3429; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Streptococcus protein for the treatment or prevention of or disease caused by Streptococcus bacteria, such as meningit
                                                                                                                Sequence
                                                                                                                                                    Streptococcus proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tettelin H;
                                                           Local
                                       72;
                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABN67435
                                                                                                                327 AA;
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              relates to a protein (ABP25413-ABP30895)
                                                         12.9%;
22.6%;
                                     55;
                                                         Score 180.5; DB : Pred. No. 6.7e-11
                                       Mismatches
                                                                           DB 23;
                                         110;
                                       Indels
                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                              rom group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infection
                                       Gaps
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115
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                                                                                                                                                                                                                                                                                     125 MRSTKSRHAGPFD------LDRLLFETNLCHQSIFYRRELFDGIGPYNLRY---
                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                         65
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RKYFKTILFNNRISVKEK 299
                                        RLALRTRLIRVKAVSKER
                                                                             -LYFFEAIQNNIVFINLNFPHNTSLISAVIYNEVFGGIDICGKMIDFKLYDTVDYYRKKY
                                                                                                                        PMYFWVA----
                                                                                                                                                               NLLSNPYPEGKIHEDMDTTFKLISCASKIA-VCDIVTA----VVYFSDNSTTRTKFNERM
                                                                                                                                                                                                                                                 LTS----IGNFUNTYNTSINSQYLKEIKLYTLEVALEEMYYGKTY--GVSPLAKLYPRS
                                                                                                                                                                                                                                                                                                                                FYQENRGQSYARNNGVLRCTGDWIAFLDSDD-YYLPYSIEVM-----YNIQKATNADIV
                                                                                                                                                                                                                                                                                                                                                                       HSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYGDVV 124
                                                                                                                                                                                                                                                                                                                                                                                                                  LISIIVPVYNGEIYIGRCLDSILEQTYQNLEIIIIDDGSSDRTGDICEKYFLE-DRRIKY
                                                                                                                                                                                                        RVWADWDFNIRCFSNPALITRYMDVVISEYNDMTGFSMRQGTDKEFRKRL
                                                                                                                      GWETCRRMLAF-LKD----KENR
                                                                                                                                                               222
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                                                                                                                                                                                                                                                                                       169
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AAY68976
ID AAY68
XX AAY68
AC AAY66
XX AAY66
XX

30-MAY-2000

(first

entry)

AAY68976;

AAY68976 standard;

Protein;

278

Cps1K

protein

which

has glycosyltransferase activity.

Capsular gene cluster; serotype 1; polysaccharide biosynthesis; capsular component; antigen; regulation; chain length determina complement-mediated opsonophagocytosis; serotype-specific detec

determination; lfic detection;

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RESULT 15
AAY68963
ID AAY68
XX
AC AAY68
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus suis serotype 1. The genes in this cluster are involved in polysaccharide biosynthesis of capsular components and antigens. The proteins have glycosyltransferase activities (CpsIE, CpsIG, CpsII, CpsIJ, CpsIJ, and CP polymerase activities (CpsIH). The capsule confers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid containing the capsular gene cluster of Streptococcus suis, used for serotype-specific detection and to generate antigens or
                                   AAY68963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e.g. against S. suis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene cluster is used as a source of probes and primers for serotype-specific detection of S. suls and is also useful i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The proteins AAY68970-76 are encoded by the capsular gene cluster of Streptococcus suis serotype 1. The genes in this cluster are involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-195104/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus suis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigen; vaccine; Streptococcal disease; CpslE; CpslF; CpslG;
CpslH; CpslI; CpslX; glycosyltransferase; CP polymerase
                                                                            AAY68963 standard; Protein; 334 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        recombinant production of the proteins. for producing antigens that can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mutants for vaccination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bacterium resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DIEN-) STICHTING DIENST LANDBOUWKUNDIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUL-1998;
22-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200005378-A2
                                                                                                                                                                                                                                                                                        171
                                                                                                                                                                                              223
                                                                                                                                                                                                                                                                                                                                   157
                                                                                                                                                                                                                                                                                                                                                                                122
                                                                                                                                                                                                                                                                                                                                                                                                                             110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eradicating a Streptococcal disease,
                                                                                                                                                                                                                                         TDKEF---
                                                                                                                                                                                                                                                                                                                                                                                                                      LGDHAASHLVYGDVVMRSTKSRHAGPFDLDRLLFETNLC-----HQSI-----FYRR 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLY------EPTTLAQVAAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISKISIIVPIYNVEKYLSKCIDSIVNQTYKHIEILLVNDGSTDNSEEICLAYAKK-DSR
                                                                                                                                                                                           TOHREHCLLEFQNERMDFY
                                                                                                                                                                                                                                                                                 ELFE-----DFRFEKGKIHEDEYFTYRLLYELEKVAIVKECLYYYVDRENSITTSSM---
                                                                                                                                                                                                                                                                                                                              ELFDGIGPYNLRY - - - RVWADWDFNIRC - - - FSNPALITRYMDVVISEYNDMTGFSMRQG
                                                                                                                                                                                                                                                                                                                                                                         DRVDASGHELTAEPLPTN-------QAVLSGRNVCKKLLEADGHREVVACNKLYKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRYFKKENGGLSDARNYGISRAKGDYLAFIDSDDFIHSEFIQRLHEAIERENALVAVAGY 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAPVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ60930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fig 4; 144pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                      ----RKRLPMY 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98EP-0202465.
98EP-0202467.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement-mediated opsonophagocytosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 179; DB 21; Pred. No. 7.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in vaccines, for cont
in humans or animals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The proteins are then useful in vaccines, for controlling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ONDERZOE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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    В
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Best Local S
Matches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The process street of capsular components and antigens. The in polysaccharide biosynthesis of capsular components and antigens. The proteins are involved in regulation (CpsA), chain length determination (CpsB, CpsC), export (CpsC), and biosynthesis (CpsE, CpsF, CpsG, CpsH, CpsJ, CpsK). The capsula confers bacterium resistance to complement-mediated opsonophagocytosis. The gene cluster is used as a source of probes and primers for serotype-specific detection of S. suis and is also useful for recombinant production of the proteins of the proteins are then useful for producing antigens that can be used in vaccines, for controlling or eradicating a Streptococcal disease, in humans or animals, e.g. against S. suis in pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           capsular component; antigen; regulation; chain length determination; complement-mediated opsonophagocytosis; serotype-specific detection; antigen; vaccine; Streptococcal disease; ORF 2Z; ORF 2Z; ORF 2Z; Cps2B; Cp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The proteins AAY68950-69 are encoded by the capsular gene cluster of Streptococcus suis serotype 2. The genes in this cluster are involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid containing the capsular gene cluster of Streptococcus suis, used for serotype-specific detection and to generate antigens or mutants for vaccination -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-195104/17.
N-PSDB; AAZ60929.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus suis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cps2K protein which has glycosyltransferase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 3; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith HE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUL-1998;
22-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOE.
                                                 216
                                                                                                                                            162
                                                                                                                                                                                       124
                                                                                                                                                                                                                                    115
    225
                                                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                                                                                                                                                                                         G
                                                                                                                                                                                                                                                                                                                                                                                                               7 SIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLVVHS 66
                                                                                                                                                                                                                                                                          KENGGLSDARNYGISRAKGDYLAFIDSDDFIHSEFIQRLHEAIERENALVAVAGYDRVDA 123
                                                                                                                                                                                                                                                                                                                                                                    SIIVPIXNVEQXLSKCINSIVNQTXKHIEILLVNDGSTDNSEEICLAYAKK-DSRIRYFK 63
HCLLEFQNERMDFYESRGDKELLLECYRSFLAFAVLFLGKYNHWLSKQQ--KKLLQTLFR
                                                 ------RKRLPMY---
                                                                                               ----DFRFEKGKIHEDEYFTYRLLYELEKVAIVKECLYYYVDRENSIITSSM---TDHRF
                                                                                                                                       IGPYNLRY---RVWADWDENIRC---FSNPALITRYMDVVISEYNDMTGFSMRQGTDKEF
                                                                                                                                                                                    SGHFLTAEPLPTN------QAVLSGRNVCKKLLEADGHRFVVAWNKLYKKELFE- 171
                                                                                                                                                                                                                               ASHLVYGDVVMRSTKSRHAGPFDLDRLLFETNLC-----HQSI-----FYRRELFDG
                                                                                                                                                                                                                                                                                                                       GPDDGPYDAMNRGVGVATGEWVLFLGADDTLY-----EPTTLAQVAAFLGDHA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                            67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            334
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98EP-0202465
98EP-0202467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cps2E; Cps2F; Cps2G; Cps2H; Cps2I; Cps2J; Cps2R; Cps2S; Cps2T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 175; DB 21;
Pred. No. 2.7e-10;
7; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polysaccharide biosynthesis;
                                               ---FWVAGWETCRRML----
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Length 334; Indels

94;

Gaps

13;

282

224

161

망 236 -AFLKDKENRRLAL 248 : |:|:||| 283 IVYKQLKQNKRLAL 296

Search completed: April 17, 2003, 17:26:56 Job time: 77 secs